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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BIRKELUND, Svend
CHRISTIANSEN, Gunna
HEBSGAARD PEDERSEN, Anna-Sofie
MYGIND, Per
KNUDSEN, Katrine

(ii) TITLE OF INVENTION: SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
PNEUMONIAE

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

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(F) ZIP: 20001

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/446,677
(B) FILING DATE: 24-MAR-2000

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/DK98/00266
(B) FILING DATE: 19-JUN-1998

vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: DK 0744/97
(B) FILING DATE: 23-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: BIRKELUND=1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-628-5197
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 205...2987

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATGTCGAA GAGAGCACTA ACCAGGAAAA TTGCGATTTC ATAAACCCAC TTTATTATTA	60
AATTCTTACT TGCATCATAT AAAATAGAAA ACTCAGAGAG TCAAGATAAA AATTCTTGAC	120
AGCTGTTTTG TCATCTTTAA CTTGATTTAC TTATTTTGTT TCTATATTGA TGCGAATAGT	180
TCTCTAAAAA ACAAAGCAT TACC ATG AAG ACT TCG ATT CCT TGG GTT TTA	231
Met Lys Thr Ser Ile Pro Trp Val Leu	
1 5	
GTT TCC TCC GTG TTA GCT TTC TCA TGT CAC CTA CAG TCA CTA GCT AAC	279
Val Ser Ser Val Leu Ala Phe Ser Cys His Leu Gln Ser Leu Ala Asn	
10 15 20 25	
GAG GAA CTT TTA TCA CCT GAT GAT AGC TTT AAT GGA AAT ATC GAT TCA	327
Glu Glu Leu Leu Ser Pro Asp Asp Ser Phe Asn Gly Asn Ile Asp Ser	
30 35 40	
GGA ACG TTT ACT CCA AAA ACT TCA GCC ACA ACA TAT TCT CTA ACA GGA	375
Gly Thr Phe Thr Pro Lys Thr Ser Ala Thr Thr Tyr Ser Leu Thr Gly	
45 50 55	
GAT GTC TTC TTT TAC GAG CCT GGA AAA GGC ACT CCC TTA TCT GAC AGT	423
Asp Val Phe Phe Tyr Glu Pro Gly Lys Gly Thr Pro Leu Ser Asp Ser	
60 65 70	
TGT TTT AAG CAA ACC ACG GAC AAT CTT ACC TTC TTG GGG AAC GGT CAT	471
Cys Phe Lys Gln Thr Thr Asp Asn Leu Thr Phe Leu Gly Asn Gly His	
75 80 85	
AGC TTA ACG TTT GGC TTT ATA GAT GCT GGC ACT CAT GCA GGT GCT GCT	519
Ser Leu Thr Phe Gly Phe Ile Asp Ala Gly Thr His Ala Gly Ala Ala	
90 95 100 105	
GCA TCT ACA ACA GCA AAT AAG AAT CTT ACC TTC TCA GGG TTT TCC TTA	567
Ala Ser Thr Thr Ala Asn Lys Asn Leu Thr Phe Ser Gly Phe Ser Leu	
110 115 120	
CTG AGT TTT GAT TCC TCT CCT AGC ACA ACG GTT ACT ACA GGT CAG GGA	615
Leu Ser Phe Asp Ser Ser Pro Ser Thr Thr Val Thr Thr Gly Gln Gly	
125 130 135	
ACG CTT TCC TCA GCA GGA GGC GTA AAT TTA GAA AAT ATT CGT AAA CTT	663
Thr Leu Ser Ser Ala Gly Gly Val Asn Leu Glu Asn Ile Arg Lys Leu	
140 145 150	
GTA GTT GCT GGG AAT TTT TCT ACT GCA GAT GGT GGA GCT ATC AAA GGA	711
Val Val Ala Gly Asn Phe Ser Thr Ala Asp Gly Gly Ala Ile Lys Gly	
155 160 165	
GCG TCT TTC CTT TTA ACT GGC ACT TCT GGA GAT GCT CTT TTT AGT AAC	759
Ala Ser Phe Leu Leu Thr Gly Thr Ser Gly Asp Ala Leu Phe Ser Asn	

170					175					180					185	
AAC	TCT	TCA	TCA	ACA	AAG	GGA	GGA	GCA	ATT	GCT	ACT	ACA	GCA	GGC	GCT	807
Asn	Ser	Ser	Ser	Thr	Lys	Gly	Gly	Ala	Ile	Ala	Thr	Thr	Ala	Gly	Ala	
				190				195						200		
CGC	ATA	GCA	AAT	AAC	ACA	GGT	TAT	GTT	AGA	TTC	CTA	TCT	AAC	ATA	GCG	855
Arg	Ile	Ala	Asn	Asn	Thr	Gly	Tyr	Val	Arg	Phe	Leu	Ser	Asn	Ile	Ala	
			205					210					215			
TCT	ACG	TCA	GGA	GGC	GCT	ATC	GAT	GAT	GAA	GGC	ACG	TCG	ATA	CTA	TCG	903
Ser	Thr	Ser	Gly	Gly	Ala	Ile	Asp	Asp	Glu	Gly	Thr	Ser	Ile	Leu	Ser	
		220					225					230				
AAC	AAC	AAA	TTT	CTA	TAT	TTT	GAA	GGG	AAT	GCA	GCG	AAA	ACT	ACT	GGC	951
Asn	Asn	Lys	Phe	Leu	Tyr	Phe	Glu	Gly	Asn	Ala	Ala	Lys	Thr	Thr	Gly	
	235					240				245						
GGT	GCG	ATC	TGC	AAC	ACC	AAG	GCG	AGT	GGA	TCT	CCT	GAA	CTG	ATA	ATC	999
Gly	Ala	Ile	Cys	Asn	Thr	Lys	Ala	Ser	Gly	Ser	Pro	Glu	Leu	Ile	Ile	
250					255				260						265	
TCT	AAC	AAT	AAG	ACT	CTG	ATC	TTT	GCT	TCA	AAC	GTA	GCA	GAA	ACA	AGC	1047
Ser	Asn	Asn	Lys	Thr	Leu	Ile	Phe	Ala	Ser	Asn	Val	Ala	Glu	Thr	Ser	
				270				275						280		
GGT	GGC	GCC	ATC	CAT	GCT	AAA	AAG	CTA	GCC	CTT	TCC	TCT	GGA	GGC	TTT	1095
Gly	Gly	Ala	Ile	His	Ala	Lys	Lys	Leu	Ala	Leu	Ser	Ser	Gly	Gly	Phe	
			285					290					295			
ACA	GAG	TTT	CTA	CGA	AAT	AAT	GTC	TCA	TCA	GCA	ACT	CCT	AAG	GGG	GGT	1143
Thr	Glu	Phe	Leu	Arg	Asn	Asn	Val	Ser	Ser	Ala	Thr	Pro	Lys	Gly	Gly	
		300					305					310				
GCT	ATC	AGC	ATC	GAT	GCC	TCA	GGA	GAG	CTC	AGT	CTT	TCT	GCA	GAG	ACA	1191
Ala	Ile	Ser	Ile	Asp	Ala	Ser	Gly	Glu	Leu	Ser	Leu	Ser	Ala	Glu	Thr	
	315					320					325					
GGA	AAC	ATT	ACC	TTT	GTA	AGA	AAT	ACC	CTT	ACA	ACA	ACC	GGA	AGT	ACC	1239
Gly	Asn	Ile	Thr	Phe	Val	Arg	Asn	Thr	Leu	Thr	Thr	Thr	Gly	Ser	Thr	
330					335				340						345	
GAT	ACT	CCT	AAA	CGT	AAT	GCG	ATC	AAC	ATA	GGA	AGT	AAC	GGG	AAA	TTC	1287
Asp	Thr	Pro	Lys	Arg	Asn	Ala	Ile	Asn	Ile	Gly	Ser	Asn	Gly	Lys	Phe	
				350				355						360		
ACG	GAA	TTA	CGG	GCT	GCT	AAA	AAT	CAT	ACA	ATT	TTC	TTC	TAT	GAT	CCC	1335
Thr	Glu	Leu	Arg	Ala	Ala	Lys	Asn	His	Thr	Ile	Phe	Phe	Tyr	Asp	Pro	
			365					370					375			
ATC	ACT	TCA	GAA	GGA	ACC	TCA	TCA	GAC	GTA	TTG	AAG	ATA	AAT	AAC	GGC	1383
Ile	Thr	Ser	Glu	Gly	Thr	Ser	Ser	Asp	Val	Leu	Lys	Ile	Asn	Asn	Gly	
		380					385					390				
TCT	GCG	GGA	GCT	CTC	AAT	CCA	TAT	CAA	GGA	ACG	ATT	CTA	TTT	TCT	GGA	1431
Ser	Ala	Gly	Ala	Leu	Asn	Pro	Tyr	Gln	Gly	Thr	Ile	Leu	Phe	Ser	Gly	
	395					400					405					

GAA ACC CTA ACA GCA GAT GAA CTT AAA GTT GCT GAC AAT TTA AAA TCT Glu Thr Leu Thr Ala Asp Glu Leu Lys Val Ala Asp Asn Leu Lys Ser 410 415 420 425	1479
TCA TTC ACG CAG CCA GTC TCC CTA TCC GGA GGA AAG TTA TTG CTA CAA Ser Phe Thr Gln Pro Val Ser Leu Ser Gly Gly Lys Leu Leu Leu Gln 430 435 440	1527
AAG GGA GTC ACT TTA GAG AGC ACG AGC TTC TCT CAA GAG GCC GGT TCT Lys Gly Val Thr Leu Glu Ser Thr Ser Phe Ser Gln Glu Ala Gly Ser 445 450 455	1575
CTC CTC GGC ATG GAT TCA GGA ACG ACA TTA TCA ACT ACA GCT GGG AGT Leu Leu Gly Met Asp Ser Gly Thr Thr Leu Ser Thr Thr Ala Gly Ser 460 465 470	1623
ATT ACA ATC ACG AAC CTA GGA ATC AAT GTT GAC TCC TTA GGT CTT AAG Ile Thr Ile Thr Asn Leu Gly Ile Asn Val Asp Ser Leu Gly Leu Lys 475 480 485	1671
CAG CCC GTC AGC CTA ACA GCA AAA GGT GCT TCA AAT AAA GTG ATC GTA Gln Pro Val Ser Leu Thr Ala Lys Gly Ala Ser Asn Lys Val Ile Val 490 495 500 505	1719
TCT GGG AAG CTC AAC CTG ATT GAT ATT GAA GGG AAC ATT TAT GAA AGT Ser Gly Lys Leu Asn Leu Ile Asp Ile Glu Gly Asn Ile Tyr Glu Ser 510 515 520	1767
CAT ATG TTC AGC CAT GAC CAG CTC TTC TCT CTA TTA AAA ATC ACG GTT His Met Phe Ser His Asp Gln Leu Phe Ser Leu Leu Lys Ile Thr Val 525 530 535	1815
GAT GCT GAT GTT GAT ACT AAC GTT GAC ATC AGC AGC CTT ATC CCT GTT Asp Ala Asp Val Asp Thr Asn Val Asp Ile Ser Ser Leu Ile Pro Val 540 545 550	1863
CCT GCT GAG GAT CCT AAT TCA GAA TAC GGA TTC CAA GGA CAA TGG AAT Pro Ala Glu Asp Pro Asn Ser Glu Tyr Gly Phe Gln Gly Gln Trp Asn 555 560 565	1911
GTT AAT TGG ACT ACG GAT ACA GCT ACA AAT ACA AAA GAG GCC ACG GCA Val Asn Trp Thr Thr Asp Thr Ala Thr Asn Thr Lys Glu Ala Thr Ala 570 575 580 585	1959
ACT TGG ACC AAA ACA GGA TTT GTT CCC AGC CCC GAA AGA AAA TCT GCG Thr Trp Thr Lys Thr Gly Phe Val Pro Ser Pro Glu Arg Lys Ser Ala 590 595 600	2007
TTA GTA TGC AAT ACC CTA TGG GGA GTC TTT ACT GAC ATT CGC TCT CTG Leu Val Cys Asn Thr Leu Trp Gly Val Phe Thr Asp Ile Arg Ser Leu 605 610 615	2055
CAA CAG CTT GTA GAG ATC GGC GCA ACT GGT ATG GAA CAC AAA CAA GGT Gln Gln Leu Val Glu Ile Gly Ala Thr Gly Met Glu His Lys Gln Gly 620 625 630	2103
TTC TGG GTT TCC TCC ATG ACG AAC TTC CTG CAT AAG ACT GGA GAT GAA Phe Trp Val Ser Ser Met Thr Asn Phe Leu His Lys Thr Gly Asp Glu	2151

635	640	645	
AAT CGC AAA GGC TTC CGT CAT ACC TCT GGA GGC TAC GTC ATC GGT GGA Asn Arg Lys Gly Phe Arg His Thr Ser Gly Gly Tyr Val Ile Gly Gly 650 655 660 665			2199
AGT GCT CAC ACT CCT AAA GAC GAC CTA TTT ACC TTT GCG TTC TGC CAT Ser Ala His Thr Pro Lys Asp Asp Leu Phe Thr Phe Ala Phe Cys His 670 675 680			2247
CTC TTT GCT AGA GAC AAA GAT TGT TTT ATC GCT CAC AAC AAC TCT AGA Leu Phe Ala Arg Asp Lys Asp Cys Phe Ile Ala His Asn Asn Ser Arg 685 690 695			2295
ACC TAC GGT GGA ACT TTA TTC TTC AAG CAC TCT CAT ACC CTA CAA CCC Thr Tyr Gly Gly Thr Leu Phe Phe Lys His Ser His Thr Leu Gln Pro 700 705 710			2343
CAA AAC TAT TTG AGA TTA GGA AGA GCA AAG TTT TCT GAA TCA GCT ATA Gln Asn Tyr Leu Arg Leu Gly Arg Ala Lys Phe Ser Glu Ser Ala Ile 715 720 725			2391
GAA AAA TTC CCT AGG GAA ATT CCC CTA GCC TTG GAT GTC CAA GTT TCG Glu Lys Phe Pro Arg Glu Ile Pro Leu Ala Leu Asp Val Gln Val Ser 730 735 740 745			2439
TTC AGC CAT TCA GAC AAC CGT ATG GAA ACG CAC TAT ACC TCA TTG CCA Phe Ser His Ser Asp Asn Arg Met Glu Thr His Tyr Thr Ser Leu Pro 750 755 760			2487
GAA TCC GAA GGT TCT TGG AGC AAC GAG TGT ATA GCT GGT GGT ATC GGC Glu Ser Glu Gly Ser Trp Ser Asn Glu Cys Ile Ala Gly Gly Ile Gly 765 770 775			2535
CTA GAC CTT CCT TTT GTT CTT TCC AAC CCA CAT CCT CTT TTC AAG ACC Leu Asp Leu Pro Phe Val Leu Ser Asn Pro His Pro Leu Phe Lys Thr 780 785 790			2583
TTC ATT CCA CAG ATG AAA GTC GAA ATG GTT TAT GTA TCA CAA AAT AGC Phe Ile Pro Gln Met Lys Val Glu Met Val Tyr Val Ser Gln Asn Ser 795 800 805			2631
TTC TTC GAA AGC TCT AGT GAT GGC CGT GGT TTT AGT ATT GGA AGG CTG Phe Phe Glu Ser Ser Ser Asp Gly Arg Gly Phe Ser Ile Gly Arg Leu 810 815 820 825			2679
CTT AAC CTC TCG ATT CCT GTG GGT GCG AAA TTC GTG CAG GGG GAT ATC Leu Asn Leu Ser Ile Pro Val Gly Ala Lys Phe Val Gln Gly Asp Ile 830 835 840			2727
GGA GAT TCC TAC ACC TAT GAT CTC TCA GGA TTC TTT GTT TCC GAT GTC Gly Asp Ser Tyr Thr Tyr Asp Leu Ser Gly Phe Phe Val Ser Asp Val 845 850 855			2775
TAT CGT AAC AAT CCC CAA TCT ACA GCG ACT CTT GTG ATG AGC CCA GAC Tyr Arg Asn Asn Pro Gln Ser Thr Ala Thr Leu Val Met Ser Pro Asp 860 865 870			2823

TCT TGG AAA ATT CGC GGT GGC AAT CTT TCA AGA CAG GCA TTT TTA CTG	2871
Ser Trp Lys Ile Arg Gly Gly Asn Leu Ser Arg Gln Ala Phe Leu Leu	
875 880 885	
AGG GGT AGC AAC AAC TAC GTC TAC AAC TCC AAT TGT GAG CTC TTC GGA	2919
Arg Gly Ser Asn Asn Tyr Val Tyr Asn Ser Asn Cys Glu Leu Phe Gly	
890 895 900 905	
CAT TAC GCT ATG GAA CTC CGT GGA TCT TCA AGG AAC TAC AAT GTA GAT	2967
His Tyr Ala Met Glu Leu Arg Gly Ser Ser Arg Asn Tyr Asn Val Asp	
910 915 920	
GTT GGT ACC AAA CTC CGA TT CTAGATTGCT AAAACTCCCT AGTTCTTCTA GGGAG	3022
Val Gly Thr Lys Leu Arg Phe	
925	
TTTTCTCATA CTTTtaggga AATATTGCT ATAGGGAATG CTTTCCTTGC AAAGTGTAAA	3082
AAATAACATT TGTCCCTCTT CAAAAAAGAT TTCTTTTAAT AATTTCTAGT TATAATTTTA	3142
TTTTAAAAAC AGTTAAATAA TTAATAGACA ATAATCTATT CTTATTGACT TCTTTTTT	3200

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Thr Ser Ile Pro Trp Val Leu Val Ser Ser Val Leu Ala Phe	
1 5 10 15	
Ser Cys His Leu Gln Ser Leu Ala Asn Glu Glu Leu Leu Ser Pro Asp	
20 25 30	
Asp Ser Phe Asn Gly Asn Ile Asp Ser Gly Thr Phe Thr Pro Lys Thr	
35 40 45	
Ser Ala Thr Thr Tyr Ser Leu Thr Gly Asp Val Phe Phe Tyr Glu Pro	
50 55 60	
Gly Lys Gly Thr Pro Leu Ser Asp Ser Cys Phe Lys Gln Thr Thr Asp	
65 70 75 80	
Asn Leu Thr Phe Leu Gly Asn Gly His Ser Leu Thr Phe Gly Phe Ile	
85 90 95	
Asp Ala Gly Thr His Ala Gly Ala Ala Ala Ser Thr Thr Ala Asn Lys	
100 105 110	
Asn Leu Thr Phe Ser Gly Phe Ser Leu Leu Ser Phe Asp Ser Ser Pro	
115 120 125	
Ser Thr Thr Val Thr Thr Gly Gln Gly Thr Leu Ser Ser Ala Gly Gly	

130	135	140
Val Asn Leu Glu Asn Ile Arg Lys Leu Val Val Ala Gly Asn Phe Ser		
145	150	155 160
Thr Ala Asp Gly Gly Ala Ile Lys Gly Ala Ser Phe Leu Leu Thr Gly		
	165	170 175
Thr Ser Gly Asp Ala Leu Phe Ser Asn Asn Ser Ser Ser Thr Lys Gly		
	180	185 190
Gly Ala Ile Ala Thr Thr Ala Gly Ala Arg Ile Ala Asn Asn Thr Gly		
	195	200 205
Tyr Val Arg Phe Leu Ser Asn Ile Ala Ser Thr Ser Gly Gly Ala Ile		
	210	215 220
Asp Asp Glu Gly Thr Ser Ile Leu Ser Asn Asn Lys Phe Leu Tyr Phe		
	225	230 235 240
Glu Gly Asn Ala Ala Lys Thr Thr Gly Gly Ala Ile Cys Asn Thr Lys		
	245	250 255
Ala Ser Gly Ser Pro Glu Leu Ile Ile Ser Asn Asn Lys Thr Leu Ile		
	260	265 270
Phe Ala Ser Asn Val Ala Glu Thr Ser Gly Gly Ala Ile His Ala Lys		
	275	280 285
Lys Leu Ala Leu Ser Ser Gly Gly Phe Thr Glu Phe Leu Arg Asn Asn		
	290	295 300
Val Ser Ser Ala Thr Pro Lys Gly Gly Ala Ile Ser Ile Asp Ala Ser		
	305	310 315 320
Gly Glu Leu Ser Leu Ser Ala Glu Thr Gly Asn Ile Thr Phe Val Arg		
	325	330 335
Asn Thr Leu Thr Thr Thr Gly Ser Thr Asp Thr Pro Lys Arg Asn Ala		
	340	345 350
Ile Asn Ile Gly Ser Asn Gly Lys Phe Thr Glu Leu Arg Ala Ala Lys		
	355	360 365
Asn His Thr Ile Phe Phe Tyr Asp Pro Ile Thr Ser Glu Gly Thr Ser		
	370	375 380
Ser Asp Val Leu Lys Ile Asn Asn Gly Ser Ala Gly Ala Leu Asn Pro		
	385	390 395 400
Tyr Gln Gly Thr Ile Leu Phe Ser Gly Glu Thr Leu Thr Ala Asp Glu		
	405	410 415
Leu Lys Val Ala Asp Asn Leu Lys Ser Ser Phe Thr Gln Pro Val Ser		
	420	425 430
Leu Ser Gly Gly Lys Leu Leu Leu Gln Lys Gly Val Thr Leu Glu Ser		
	435	440 445

Thr	Ser	Phe	Ser	Gln	Glu	Ala	Gly	Ser	Leu	Leu	Gly	Met	Asp	Ser	Gly	
450						455					460					
Thr	Thr	Leu	Ser	Thr	Thr	Ala	Gly	Ser	Ile	Thr	Ile	Thr	Asn	Leu	Gly	
465					470					475					480	
Ile	Asn	Val	Asp	Ser	Leu	Gly	Leu	Lys	Gln	Pro	Val	Ser	Leu	Thr	Ala	
				485					490						495	
Lys	Gly	Ala	Ser	Asn	Lys	Val	Ile	Val	Ser	Gly	Lys	Leu	Asn	Leu	Ile	
			500					505					510			
Asp	Ile	Glu	Gly	Asn	Ile	Tyr	Glu	Ser	His	Met	Phe	Ser	His	Asp	Gln	
		515					520					525				
Leu	Phe	Ser	Leu	Leu	Lys	Ile	Thr	Val	Asp	Ala	Asp	Val	Asp	Thr	Asn	
	530					535					540					
Val	Asp	Ile	Ser	Ser	Leu	Ile	Pro	Val	Pro	Ala	Glu	Asp	Pro	Asn	Ser	
545					550					555					560	
Glu	Tyr	Gly	Phe	Gln	Gly	Gln	Trp	Asn	Val	Asn	Trp	Thr	Thr	Asp	Thr	
				565					570					575		
Ala	Thr	Asn	Thr	Lys	Glu	Ala	Thr	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Phe	
			580					585						590		
Val	Pro	Ser	Pro	Glu	Arg	Lys	Ser	Ala	Leu	Val	Cys	Asn	Thr	Leu	Trp	
		595					600					605				
Gly	Val	Phe	Thr	Asp	Ile	Arg	Ser	Leu	Gln	Gln	Leu	Val	Glu	Ile	Gly	
	610					615					620					
Ala	Thr	Gly	Met	Glu	His	Lys	Gln	Gly	Phe	Trp	Val	Ser	Ser	Met	Thr	
625					630					635					640	
Asn	Phe	Leu	His	Lys	Thr	Gly	Asp	Glu	Asn	Arg	Lys	Gly	Phe	Arg	His	
				645					650					655		
Thr	Ser	Gly	Gly	Tyr	Val	Ile	Gly	Gly	Ser	Ala	His	Thr	Pro	Lys	Asp	
			660					665					670			
Asp	Leu	Phe	Thr	Phe	Ala	Phe	Cys	His	Leu	Phe	Ala	Arg	Asp	Lys	Asp	
		675					680					685				
Cys	Phe	Ile	Ala	His	Asn	Asn	Ser	Arg	Thr	Tyr	Gly	Gly	Thr	Leu	Phe	
	690					695					700					
Phe	Lys	His	Ser	His	Thr	Leu	Gln	Pro	Gln	Asn	Tyr	Leu	Arg	Leu	Gly	
705					710					715					720	
Arg	Ala	Lys	Phe	Ser	Glu	Ser	Ala	Ile	Glu	Lys	Phe	Pro	Arg	Glu	Ile	
				725					730					735		
Pro	Leu	Ala	Leu	Asp	Val	Gln	Val	Ser	Phe	Ser	His	Ser	Asp	Asn	Arg	
			740					745					750			

Met Glu Thr His Tyr Thr Ser Leu Pro Glu Ser Glu Gly Ser Trp Ser
755 760 765

Asn Glu Cys Ile Ala Gly Gly Ile Gly Leu Asp Leu Pro Phe Val Leu
770 775 780

Ser Asn Pro His Pro Leu Phe Lys Thr Phe Ile Pro Gln Met Lys Val
785 790 795 800

Glu Met Val Tyr Val Ser Gln Asn Ser Phe Phe Glu Ser Ser Ser Asp
805 810 815

Gly Arg Gly Phe Ser Ile Gly Arg Leu Leu Asn Leu Ser Ile Pro Val
820 825 830

Gly Ala Lys Phe Val Gln Gly Asp Ile Gly Asp Ser Tyr Thr Tyr Asp
835 840 845

Leu Ser Gly Phe Phe Val Ser Asp Val Tyr Arg Asn Asn Pro Gln Ser
850 855 860

Thr Ala Thr Leu Val Met Ser Pro Asp Ser Trp Lys Ile Arg Gly Gly
865 870 875 880

Asn Leu Ser Arg Gln Ala Phe Leu Leu Arg Gly Ser Asn Asn Tyr Val
885 890 895

Tyr Asn Ser Asn Cys Glu Leu Phe Gly His Tyr Ala Met Glu Leu Arg
900 905 910

Gly Ser Ser Arg Asn Tyr Asn Val Asp Val Gly Thr Lys Leu Arg Phe
915 920 925

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAATCGC	AATTTTCCTG	GTTAGTGCTC	TCTTCGACAT	TGGCATGTTT	TACTAGTTGT	60
TCCACTGTTT	TTGCTGCAAC	TGCTGAAAAT	ATAGGCCCCCT	CTGATAGCTT	TGACGGAAGT	120
ACTAACACAG	GCACCTATAC	TCCTAAAAAT	ACGACTACTG	GAATAGACTA	TACTCTGACA	180
GGAGATATAA	CTCTGCAAAA	CCTTGGGGAT	TCGGCAGCTT	TAACGAAGGG	TTGTTTTTCT	240
GACACTACGG	AATCTTTAAG	CTTTGCCGGT	AAGGGGTACT	CACTTTCTTT	TTTAAATATT	300
AAGTCTAGTG	CTGAAGGCGC	AGCACTTTCT	GTTACAACCTG	ATAAAAATCT	GTCGCTAACA	360
GGATTTTCGA	GTCTTACTTT	CTTAGCGGCC	CCATCATCGG	TAATCACAAC	CCCCTCAGGA	420
AAAGGTGCAG	TTAAATGTGG	AGGGGATCTT	ACATTTGATA	ACAATGGAAC	TATTTTATTT	480
AAACAAGATT	ACTGTGAGGA	AAATGGCGGA	GCCATTTCTA	CCAAGAATCT	TTCTTTGAAA	540
AACAGCACGG	GATCGATTTT	TTTTGAAGGG	AATAAATCGA	GCGCAACAGG	GAAAAAAGGT	600
GGGGCTATTT	GTGCTACTGG	TACTGTAGAT	ATTACAAATA	ATACGGCTCC	TACCCTCTTC	660
TCGAACAATA	TTGCTGAAGC	TGCAGGTGGA	GCTATAAATA	GCACAGGAAA	CTGTACAATT	720
ACAGGGAATA	CGTCTCTTGT	ATTTTCTGAA	AATAGTGTGA	CAGCGACCGC	AGGAAATGGA	780

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GGAGCTCTTT CTGGAGATGC CGATGTTACC ATATCTGGGA ATCAGAGTGT AACTTTCTCA      840
GGAAACCAAG CTGTAGCTAA TGGCGGAGCC ATTTATGCTA AGAAGCTTAC ACTGGCTTCC      900
GGGGGGGGGG GGGGTATCTC CTTTTCTAAC AATATAGTCC AAGGTACCAC TGCAGGTAAT      960
GGTGGAGCCA TTTCTATACT GGCAGCTGGA GAGTGTAGTC TTTCAGCAGA AGCAGGGGAC     1020
ATTACCTTCA ATGGGAATGC CATTGTTGCA ACTACACCAC AAAC TACAAA AAGAAATTCT     1080
ATTGACATAG GATCTACTGC AAAGATCACG AATTTACGTG CAATATCTGG GCATAGCATC     1140
TTTTTCTACG ATCCGATTAC TGCTAATACG GCTGCGGATT CTACAGATAC TTAAATCTC      1200
AATAAGGCTG ATGCAGGTAA TAGTACAGAT TATAGTGGGT CGATTGTTTT TTCTGGTGAA      1260
AAGCTCTCTG AAGATGAAGC AAAAGTTGCA GACAACCTCA CTTCTACGCT GAAGCAGCCT     1320
GTAAC TCTAA CTGCAGGAAA TTTAGTACTT AAACGTGGTG TCACTCTCGA TACGAAAGGC     1380
TTTACTCAGA CCGCGGGTTC CTCTGTTATT ATGGATGCGG GCACAACGTT AAAAGCAAGT     1440
ACAGAGGAGG TCACTTTAAC AGGTCTTTCC ATTCCTGTAG ACTCTTTAGG CGAGGGTAAG     1500
AAAGTTGTAA TTGCTGCTTC TGCAGCAAGT AAAAATGTAG CCCTTAGTGG TCCGATTCTT     1560
CTTTTGGATA ACCAAGGGAA TGCTTATGAA AATCAGCACT TAGGAAAAAC TCAAGACTTT     1620
TCATTTGTGC AGCTCTCTGC TCTGGGTA CTGCAACACTA CAGATGTTCC AGCGGTTTCT     1680
ACAGTAGCAA CTCCTACGCA CTATGGGTAT CAAGGTACTT GGGGAATGAC TTGGGTTGAT     1740
GATACCGCAA GCACTCCAAA GACTAAGACA GCGACATTAG CTTGGACCAA TACAGGCTAC     1800
CTTCCGAATC CTGAGCGTCA AGGACCTTTA GTTCCTAATA GCCTTTGGGG ATCTTTTTCA     1860
GACATCCAAG CGATTCAAGG TGTCATAGAG AGAAGTGCTT TGACTCTTTG TTCAGATCGA     1920
GGCTTCTGGG CTGCGGGAGT CGCCAATTTC TTAGATAAAG ATAAGAAAGG GGAAAAACGC     1980
AAATACCGTC ATAAATCTGG TGGATATGCT ATCGGAGGTG CAGCGCAAAC TTGTTCTGAA     2040
AACTTAATTA GCTTTGCCTT TTGCCAACTC TTTGGTAGCG ATAAAGATTT CTTAGTCGCT     2100
AAAAATCATA CTGATACCTA TGCAGGAGCC TTCTATATCC AACACATTAC AGAATGTAGT     2160
GGGTTCATAG GTTGTCTCTT AGATAAACTT CCTGGCTCTT GGAGTCATAA ACCCCTCGTT     2220
TTAGAAGGGG AGCTCGCTTA TAGCCACGTC AGTAATGATC TGAAGACAAA GTATACTGCG     2280
TATCCTGAGG TGAAGGTTT TGGGGGAAT AATGCTTTTA ACATGATGTT GGGAGCTTCT     2340
TCTCATTTCT ATCCTGAATA CCTGCATTGT TTTGATACCT ATGCTCCATA CATCAA CTG     2400
AATCTGACCT ATATACGTCA GGACAGCTTC TCGGAGAAAG GTACAGAAGG AAGATCTTTT     2460
GATGACAGCA ACCTCTTCAA TTTATCTTTG CCTATAGGGG TGAAGTTTGA GAAGTTCTCT     2520
GATTGTAATG ACTTTTCTTA TGATCTGACT TTATCCTATG TTCCTGATCT TATCCGCAAT     2580
GATCCCAAAT GCACTACAGC ACTTGTAATC AGCGGAGCCT CTTGGGAAAC TTATGCCAAT     2640
AACTTAGCAC GACAGGCCTT GCAAGTGCGT GCAGGCAGTC ACTACGCCTT CTCTCCTATG     2700
TTTGAAGTGC TCGGCCAGTT TGTCTTTGAA GTTCGTGGAT CCTCACGGAT TTATAATGTA     2760
GATCTTGGGG GTAAGTTCCA ATTCTAGGAG CGTCTCTCAT GTCTCAGAAA TTCTG      2815

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Lys Ser Gln Phe Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys
 1             5             10             15

Phe Thr Ser Cys Ser Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly
      20             25             30

Pro Ser Asp Ser Phe Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro
      35             40             45

Lys Asn Thr Thr Thr Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr
      50             55             60

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Leu	Gln	Asn	Leu	Gly	Asp	Ser	Ala	Ala	Leu	Thr	Lys	Gly	Cys	Phe	Ser	
65					70					75					80	
Asp	Thr	Thr	Glu	Ser	Leu	Ser	Phe	Ala	Gly	Lys	Gly	Tyr	Ser	Leu	Ser	
				85					90					95		
Phe	Leu	Asn	Ile	Lys	Ser	Ser	Ala	Glu	Gly	Ala	Ala	Leu	Ser	Val	Thr	
			100					105					110			
Thr	Asp	Lys	Asn	Leu	Ser	Leu	Thr	Gly	Phe	Ser	Ser	Leu	Thr	Phe	Leu	
		115					120					125				
Ala	Ala	Pro	Ser	Ser	Val	Ile	Thr	Thr	Pro	Ser	Gly	Lys	Gly	Ala	Val	
		130				135					140					
Lys	Cys	Gly	Gly	Asp	Leu	Thr	Phe	Asp	Asn	Asn	Gly	Thr	Ile	Leu	Phe	
145					150					155					160	
Lys	Gln	Asp	Tyr	Cys	Glu	Glu	Asn	Gly	Gly	Ala	Ile	Ser	Thr	Lys	Asn	
				165				170						175		
Leu	Ser	Leu	Lys	Asn	Ser	Thr	Gly	Ser	Ile	Ser	Phe	Glu	Gly	Asn	Lys	
			180					185					190			
Ser	Ser	Ala	Thr	Gly	Lys	Lys	Gly	Gly	Ala	Ile	Cys	Ala	Thr	Gly	Thr	
		195					200					205				
Val	Asp	Ile	Thr	Asn	Asn	Thr	Ala	Pro	Thr	Leu	Phe	Ser	Asn	Asn	Ile	
	210					215					220					
Ala	Glu	Ala	Ala	Gly	Gly	Ala	Ile	Asn	Ser	Thr	Gly	Asn	Cys	Thr	Ile	
225					230					235					240	
Thr	Gly	Asn	Thr	Ser	Leu	Val	Phe	Ser	Glu	Asn	Ser	Val	Thr	Ala	Thr	
				245					250					255		
Ala	Gly	Asn	Gly	Gly	Ala	Leu	Ser	Gly	Asp	Ala	Asp	Val	Thr	Ile	Ser	
			260					265				270				
Gly	Asn	Gln	Ser	Val	Thr	Phe	Ser	Gly	Asn	Gln	Ala	Val	Ala	Asn	Gly	
		275					280					285				
Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu	Thr	Leu	Ala	Ser	Gly	Gly	Gly	Gly	
		290				295					300					
Gly	Ile	Ser	Phe	Ser	Asn	Asn	Ile	Val	Gln	Gly	Thr	Thr	Ala	Gly	Asn	
305					310					315					320	
Gly	Gly	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Gly	Glu	Cys	Ser	Leu	Ser	Ala	
				325					330					335		
Glu	Ala	Gly	Asp	Ile	Thr	Phe	Asn	Gly	Asn	Ala	Ile	Val	Ala	Thr	Thr	
			340					345					350			
Pro	Gln	Thr	Thr	Lys	Arg	Asn	Ser	Ile	Asp	Ile	Gly	Ser	Thr	Ala	Lys	
		355					360					365				

Ile Thr Asn Leu Arg Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp
 370 375 380
 Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu
 385 390 395 400
 Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val
 405 410 415
 Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn
 420 425 430
 Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu
 435 440 445
 Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr
 450 455 460
 Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser
 465 470 475 480
 Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu
 485 490 495
 Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn
 500 505 510
 Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala
 515 520 525
 Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln
 530 535 540
 Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro
 545 550 555 560
 Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met
 565 570 575
 Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr
 580 585 590
 Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly
 595 600 605
 Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala
 610 615 620
 Ile Gln Gly Val Ile Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg
 625 630 635 640
 Gly Phe Trp Ala Ala Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys
 645 650 655
 Gly Glu Lys Arg Lys Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly
 660 665 670
 Gly Ala Ala Gln Thr Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys

675		680		685
Gln Leu Phe Gly Ser Asp Lys Asp Phe Leu Val Ala Lys Asn His Thr				
690		695		700
Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His Ile Thr Glu Cys Ser				
705		710		715
Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro Gly Ser Trp Ser His				
		725		730
Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr Ser His Val Ser Asn				
		740		745
Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu Val Lys Gly Ser Trp				
		755		760
Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala Ser Ser His Ser Tyr				
		770		775
Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala Pro Tyr Ile Lys Leu				
		785		790
Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser Glu Lys Gly Thr Glu				
		805		810
Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn Leu Ser Leu Pro Ile				
		820		825
Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn Asp Phe Ser Tyr Asp				
		835		840
Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg Asn Asp Pro Lys Cys				
		850		855
Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn				
		865		870
Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala				
		885		890
Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg				
		900		905
Gly Ser Ser Arg Ile Tyr Asn Val Asp Leu Gly Gly Lys Phe Gln Phe				
		915		920
				925

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3052 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGCGATTTT	CGCTCTGCGG	ATTTCTCTCTA	GTTTTTTCTT	TAACATTGCT	CTCAGTCTTC	60
GACACTTCTT	TGAGTGCTAC	TACGATTTCT	TTAACCCAG	AAGATAGTTT	TCATGGAGAT	120
AGTCAGAATG	CAGAACGTTT	TTATAATGTT	CAAGCTGGGG	ATGTCTATAG	CCTTACTGGT	180
GATGTCTCAA	TATCTAACGT	CGATAACTCT	GCATTAAATA	AAGCCTGCTT	CAATGTGACC	240
TCAGGAAGTG	TGACGTTTCG	AGGAAATCAT	CATGGGTAT	ATTTTAATAA	TATTTCTCTCA	300
GGAACACAA	AGGAAGGGG	TGTACTTTGT	TGCCAAGATC	CTCAAGCAAC	GGCACGTTTT	360
TCTGGGTTCT	CCACGCTCTC	TTTTATTCTC	AGCCCCGGAG	ATATTAAAGA	ACAGGGATGT	420
CTCTATTCAA	AAAATGCACT	TATGCTCTTA	AACAATTATG	TAGTGCGTTT	TGAACAAAAC	480
CAAAGTAAGA	CTAAAGGCGG	AGCTATTAGT	GGGGCGAATG	TTACTATAGT	AGGCAACTAC	540
GATTCGCTCT	CTTTCTATCA	GAATGCAGCC	ACTTTTGGAG	GTGCTATCCA	TTCTTCAGGT	600
CCCCTACAGA	TTGCAGTAAA	TCAGGCAGAG	ATAAGATTTG	CACAAAATAC	TGCCAAGAAT	660
GGTTCTGGAG	GGGCTTTGTA	CTCCGATGGT	GATATTGATA	TTGATCAGAA	TGCTTATGTT	720
CTATTTTCGAG	AAAATGAGGC	ATTGACTACT	GCTATAGGTA	AGGGAGGGGC	TGTCTGTTGT	780
CTTCCCCTT	CAGGAAGTAG	TACTCCAGTT	CCTATTGTGA	CTTTCTCTGA	CAATAAACAG	840
TTAGTCTTTG	AAAGAAACCA	TTCCATAATG	GGTGGCGGAG	CCATTTATGC	TAGGAAACTT	900
AGCATCTCTT	CAGGAGGTCC	TACTCTATTT	ATCAATAATA	TATCATATGC	AAATTGCAA	960
AATTTAGGTG	GAGCTATTGC	CATTGATACT	GGAGGGGAGA	TCAGTTTATC	AGCAGAGAAA	1020
GGAACAATTA	CATTCCAAGG	AAACCGGACG	AGCTTACCGT	TTTTGAATGG	CATCCATCTT	1080
TTACAAAATG	CTAAATTCCT	GAAATTACAG	GCGAGAAATG	GATGCTCTAT	AGAATTTTAT	1140
GATCCTATTA	CTTCTGAAGC	AGATGGGTCT	ACCCAATTGA	ATATCAACGG	AGATCCTAAA	1200
AATAAAGAGT	ACACAGGGAC	CATACTCTTT	TCTGGAGAAA	AGAGTCTAGC	AAACGATCCT	1260
AGGGATTTTA	AATCTACAAT	CCCTCAGAAC	GTCAACCTGT	CTGCAGGATA	CTTAGTTATT	1320
AAAGAGGGGG	CCGAAGTCAC	AGTTTCAAAA	TTCACGCAGT	CTCCAGGATC	GCATTTAGTT	1380
TTAGATTTAG	GAACCAAACT	GATAGCCTCT	AAGGAAGACA	TTGCCATCAC	AGGCCTCGCG	1440
ATAGATATAG	ATAGCTTAAG	CTCATCCTCA	ACAGCAGCTG	TTATTAAAGC	AAACACCGCA	1500
AATAAACAGA	TATCCGTGAC	GGACTCTATA	GAACCTATCT	CGCCTACTGG	CAATGCCTAT	1560
GAAGATCTCA	GAATGAGAAA	TTCACAGACG	TTCCCTCTGC	TCTCTTTAGA	GCCTGGAGCC	1620
GGGGGTAGTG	TGACTGTAAC	TGCTGGAGAT	TTCTTACCGG	TAAGTCCCCA	TTATGGTTTT	1680
CAAGGCAATT	GGAAATTAGC	TTGGACAGGA	ACTGGAAACA	AAGTTGGAGA	ATTCTTCTGG	1740
GATAAAATAA	ATTATAAGCC	TAGACCTGAA	AAAGAAGGAA	ATTTAGTTCC	TAATATCTTG	1800
TGGGGGAATG	CTGTAAATGT	CAGATCCTTA	ATGCAGGTTT	AAGAGACCCA	TGCATCGAGC	1860
TTACAGACAG	ATCGAGGGCT	GTGGATCGAT	GGAAATGGGA	ATTTCTTCCA	TGTATCTGCC	1920
TCCGAAGACA	ATAAAGGTA	CCGTATAAC	AGCGGTGGAT	ATGTTCTATC	TGTAAATAAT	1980
GAGATCACAC	CTAAGCACTA	TACTTCGATG	GCATTTTCCC	AACTCTTTAG	TAGAGACAAG	2040
GACTATGCGG	TTTCCAACAA	CGAATACAGA	ATGTATTTAG	GATCGTATCT	CTATCAATAT	2100
ACAACCTCCC	TAGGGAATAT	TTTCCGTTAT	GCTTCGCGTA	ACCCTAATGT	AAACGTCGGG	2160
ATTCTCTCAA	GAAGGTTTCT	TCAAAATCCT	CTTATGATTT	TTCAATTTTT	GTGTGCTTAT	2220
GGTCATGCCA	CCAATGATAT	GAAAACAGAC	TACGCAAATT	TCCCTATGGT	GAAAAACAGC	2280
TGGAGAAACA	ATTGTTGGGC	TATAGAGTGC	GGAGGGAGCA	TGCCTCTATT	GGTATTTGAG	2340
AACGGAAGAC	TTTTCCAAGG	TGCCATCCCA	TTTATGAAAC	TACAATTAGT	TTATGCTTAT	2400
CAGGGAGATT	TCAAAGAGAC	GACTGCAGAT	GGCCGTAGAT	TTAGTAATGG	GAGTTTAAAC	2460
TCGATTTCTG	TACCTCTAGG	CATACGCTTT	GAGAAGCTGG	CACTTTCTCA	GGATGTACTC	2520
TATGACTTTA	GTTTCTCCTA	TATTCTGAT	ATTTTCCGTA	AGGATCCCTC	ATGTGAAGCT	2580
GCTCTGGTGA	TTAGCGGAGA	CTCCTGGCTT	GTTCCGGCAG	CACACGTATC	AAGACATGCT	2640
TTTGTAGGGA	GTGGAACGGG	TCGGTATCAC	TTTAACGACT	ATACTGAGCT	CTTATGTCTGA	2700
GGAAGTATAG	AATGCCGCCC	CCATGCTAGG	AATTATAATA	TAACTGTGG	AAGCAAATTT	2760
CGTTTTTAGA	AGGTTTCCAT	TGCCTGTGTG	GTTCCGGATC	TTAACTATAA	ATCCTGGACT	2820
ATGGATCATA	GGCATTGGGT	TTCTCGAACT	TGTGTGGAGA	ATAACGACAT	TTTATATGCA	2880
TAACGGAATA	CTCGTATCAC	CTCAGCCCCCT	AGAGACATTC	TTAGGGGTT	CTTTATTTGT	2940
CTAAACTTCG	TATTTTATCG	AGAATCCTTT	ACGTTCTTGG	TTTGCTTGTC	TCCGAGGAGT	3000
TCTCTAACGA	ATCATAGGGA	TTCCAGGGTT	CTGTTCTTGG	AGTCCTTTGG	A	3052

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 922 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Leu Thr Leu
 1           5           10           15
Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr
          20           25           30
Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr
          35           40           45
Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile
          50           55           60
Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr
          65           70           75           80
Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn
          85           90           95
Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln
          100          105          110
Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe
          115          120          125
Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys
          130          135          140
Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn
          145          150          155          160
Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile
          165          170          175
Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe
          180          185          190
Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln
          195          200          205
Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly
          210          215          220
Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val
          225          230          235          240
Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly
          245          250          255
Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile
          260          265          270

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Val	Thr	Phe	Ser	Asp	Asn	Lys	Gln	Leu	Val	Phe	Glu	Arg	Asn	His	Ser		
		275					280					285					
Ile	Met	Gly	Gly	Gly	Ala	Ile	Tyr	Ala	Arg	Lys	Leu	Ser	Ile	Ser	Ser		
	290					295					300						
Gly	Gly	Pro	Thr	Leu	Phe	Ile	Asn	Asn	Ile	Ser	Tyr	Ala	Asn	Ser	Gln		
305					310					315					320		
Asn	Leu	Gly	Gly	Ala	Ile	Ala	Ile	Asp	Thr	Gly	Gly	Glu	Ile	Ser	Leu		
				325					330					335			
Ser	Ala	Glu	Lys	Gly	Thr	Ile	Thr	Phe	Gln	Gly	Asn	Arg	Thr	Ser	Leu		
			340					345					350				
Pro	Phe	Leu	Asn	Gly	Ile	His	Leu	Leu	Gln	Asn	Ala	Lys	Phe	Leu	Lys		
		355					360					365					
Leu	Gln	Ala	Arg	Asn	Gly	Cys	Ser	Ile	Glu	Phe	Tyr	Asp	Pro	Ile	Thr		
	370					375					380						
Ser	Glu	Ala	Asp	Gly	Ser	Thr	Gln	Leu	Asn	Ile	Asn	Gly	Asp	Pro	Lys		
385					390					395					400		
Asn	Lys	Glu	Tyr	Thr	Gly	Thr	Ile	Leu	Phe	Ser	Gly	Glu	Lys	Ser	Leu		
				405					410					415			
Ala	Asn	Asp	Pro	Arg	Asp	Phe	Lys	Ser	Thr	Ile	Pro	Gln	Asn	Val	Asn		
			420					425					430				
Leu	Ser	Ala	Gly	Tyr	Leu	Val	Ile	Lys	Glu	Gly	Ala	Glu	Val	Thr	Val		
		435					440					445					
Ser	Lys	Phe	Thr	Gln	Ser	Pro	Gly	Ser	His	Leu	Val	Leu	Asp	Leu	Gly		
	450					455					460						
Thr	Lys	Leu	Ile	Ala	Ser	Lys	Glu	Asp	Ile	Ala	Ile	Thr	Gly	Leu	Ala		
465					470					475					480		
Ile	Asp	Ile	Asp	Ser	Leu	Ser	Ser	Ser	Ser	Thr	Ala	Ala	Val	Ile	Lys		
				485					490					495			
Ala	Asn	Thr	Ala	Asn	Lys	Gln	Ile	Ser	Val	Thr	Asp	Ser	Ile	Glu	Leu		
			500					505					510				
Ile	Ser	Pro	Thr	Gly	Asn	Ala	Tyr	Glu	Asp	Leu	Arg	Met	Arg	Asn	Ser		
		515					520					525					
Gln	Thr	Phe	Pro	Leu	Leu	Ser	Leu	Glu	Pro	Gly	Ala	Gly	Gly	Ser	Val		
	530					535					540						
Thr	Val	Thr	Ala	Gly	Asp	Phe	Leu	Pro	Val	Ser	Pro	His	Tyr	Gly	Phe		
545					550					555					560		
Gln	Gly	Asn	Trp	Lys	Leu	Ala	Trp	Thr	Gly	Thr	Gly	Asn	Lys	Val	Gly		
			565						570					575			
Glu	Phe	Phe	Trp	Asp	Lys	Ile	Asn	Tyr	Lys	Pro	Arg	Pro	Glu	Lys	Glu		
			580					585					590				

Gly	Asn	Leu	Val	Pro	Asn	Ile	Leu	Trp	Gly	Asn	Ala	Val	Asn	Val	Arg	595	600	605	
Ser	Leu	Met	Gln	Val	Gln	Glu	Thr	His	Ala	Ser	Ser	Leu	Gln	Thr	Asp	610	615	620	
Arg	Gly	Leu	Trp	Ile	Asp	Gly	Ile	Gly	Asn	Phe	Phe	His	Val	Ser	Ala	625	630	635	640
Ser	Glu	Asp	Asn	Ile	Arg	Tyr	Arg	His	Asn	Ser	Gly	Gly	Tyr	Val	Leu	645	650	655	
Ser	Val	Asn	Asn	Glu	Ile	Thr	Pro	Lys	His	Tyr	Thr	Ser	Met	Ala	Phe	660	665	670	
Ser	Gln	Leu	Phe	Ser	Arg	Asp	Lys	Asp	Tyr	Ala	Val	Ser	Asn	Asn	Glu	675	680	685	
Tyr	Arg	Met	Tyr	Leu	Gly	Ser	Tyr	Leu	Tyr	Gln	Tyr	Thr	Thr	Ser	Leu	690	695	700	
Gly	Asn	Ile	Phe	Arg	Tyr	Ala	Ser	Arg	Asn	Pro	Asn	Val	Asn	Val	Gly	705	710	715	720
Ile	Leu	Ser	Arg	Arg	Phe	Leu	Gln	Asn	Pro	Leu	Met	Ile	Phe	His	Phe	725	730	735	
Leu	Cys	Ala	Tyr	Gly	His	Ala	Thr	Asn	Asp	Met	Lys	Thr	Asp	Tyr	Ala	740	745	750	
Asn	Phe	Pro	Met	Val	Lys	Asn	Ser	Trp	Arg	Asn	Asn	Cys	Trp	Ala	Ile	755	760	765	
Glu	Cys	Gly	Gly	Ser	Met	Pro	Leu	Leu	Val	Phe	Glu	Asn	Gly	Arg	Leu	770	775	780	
Phe	Gln	Gly	Ala	Ile	Pro	Phe	Met	Lys	Leu	Gln	Leu	Val	Tyr	Ala	Tyr	785	790	795	800
Gln	Gly	Asp	Phe	Lys	Glu	Thr	Thr	Ala	Asp	Gly	Arg	Arg	Phe	Ser	Asn	805	810	815	
Gly	Ser	Leu	Thr	Ser	Ile	Ser	Val	Pro	Leu	Gly	Ile	Arg	Phe	Glu	Lys	820	825	830	
Leu	Ala	Leu	Ser	Gln	Asp	Val	Leu	Tyr	Asp	Phe	Ser	Phe	Ser	Tyr	Ile	835	840	845	
Pro	Asp	Ile	Phe	Arg	Lys	Asp	Pro	Ser	Cys	Glu	Ala	Ala	Leu	Val	Ile	850	855	860	
Ser	Gly	Asp	Ser	Trp	Leu	Val	Pro	Ala	Ala	His	Val	Ser	Arg	His	Ala	865	870	875	880
Phe	Val	Gly	Ser	Gly	Thr	Gly	Arg	Tyr	His	Phe	Asn	Asp	Tyr	Thr	Glu	885	890	895	

Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr
 900 905 910

Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe
 915 920

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAGATTC	CACTCCGCTT	TTTATTGATA	TCATTAGTAC	CTACGCTTTC	TATGTCGAAT	60
TTATTAGGAG	CTGCTACTAC	CGAAGAGCTA	TCGGCTAGCA	ATAGCTTCGA	TGGAAGTACA	120
TCAACAACAA	GCTTTTCTAG	TAAAACATCA	TCGGCTACAG	ATGGCACCAA	TTATGTTTTT	180
AAAGATTCTG	TAGTTATAGA	AAATGTACCC	AAAACAGGGG	AAACTCAGTC	TACTAGTTGT	240
TTTAAAAATG	ACGCTGCAGC	TGGAGATCTA	AATTTCTTAG	GAGGGGGATT	TTCTTTTCACA	300
TTTAGCAATA	TCGATGCAAC	CACGGCTTCT	GGAGCTGCTA	TTGGAAGTGA	AGCAGCTAAT	360
AAGACAGTCA	CGTTATCAGG	ATTTTCGGCA	CTTTCTTTTC	TTAAATCCCC	AGCAAGTACA	420
GTGACTAATG	GATTGGGAGC	TATCAATGTT	AAAGGGAATT	TAAGCCTATT	GGATAATGAT	480
AAGGTATTGA	TTCAGGACAA	TTTCTCAACA	GGAGATGGCG	GAGCAATTAA	TTGTGCAGGC	540
TCCTTGAAGA	TCGCAAACAA	TAAGTCCCTT	TCTTTTATTG	GAAATAGTTC	TTCAACACGT	600
GGCGGAGCGA	TTCATACCAA	AAACCTCACA	CTATCTTCTG	GTGGGGAAAC	TCTATTTTCAG	660
GGGAATACAG	CGCCTACGGC	TGCTGGTAAA	GGAGGTGCTA	TCGCGATTGC	AGACTCTGGC	720
ACCTTATCCA	TTTCTGGAGA	CAGTGGCGAC	ATTATCTTTG	AAGGCAATAC	GATAGGAGCT	780
ACAGGAACCG	TCTCTCATAG	TGCTATTGAT	TTAGGAACTA	GCGCTAAGAT	AACTGCGTTA	840
CGTGCTGCGC	AAGGACATAC	GATATACTTT	TATGATCCGA	TTACTGTAAC	AGGATCGACA	900
TCTGTTGCTG	ATGCTCTCAA	TATTAATAGC	CCTGATACTG	GAGATAACAA	AGAGTATACG	960
GGAACCATAG	TCTTTTCTGG	AGAGAAGCTC	ACGGAGGCAG	AAGCTAAAGA	TGAGAAGAAC	1020
CGCACTTCTA	AATTACTTCA	AAATGTTGCT	TTTAAAAATG	GGACTGTAGT	TTTAAAAGGT	1080
GATGTCGTTT	TAAGTGCGAA	CGGTTTCTCT	CAGGATGCAA	ACTCTAAGTT	GATTATGGAT	1140
TTAGGGACGT	CGTTGGTTGC	AAACACCGAA	AGTATCGAGT	TAACGAATTT	GGAAATTAAT	1200
ATAGACTCTC	TCAGGAACGG	GAAAAAGATA	AAACTCAGTG	CTGCCACAGC	TCAGAAAGAT	1260
ATTCGTATAG	ATCGTCCTGT	TGTACTGGCA	ATTAGCGATG	AGAGTTTTTA	TCAAATGGC	1320
TTTTTGAATG	AGGACCATTG	CTATGATGGG	ATTCTTGAGT	TAGATGCTGG	GAAAGACATC	1380
GTGATTTCTG	CAGATTCTCG	CAGTATAAAT	GCTGTACAAT	CTCCGTATGG	CTATCAGGGA	1440
AAGTGGACAA	TCAATTGGTC	TACTGATGAT	AAGAAAGCTA	CGGTTTCTTG	GGCAAAGCAA	1500
AGTTTAAATC	CCACTGCTGA	GCAGGAGGCT	CCGTTAGTTC	CTAATCTTCT	TTGGGGTTCT	1560
TTTATAGATG	TTCGTCCCTT	CCAAAATTTT	ATAGAGCTAG	GTACTGAAGG	TGCTCCTTAC	1620
GAAAAGAGAT	TTTGGGTTGC	AGGCATTTCC	AATGTTTTGC	ATAGGAGCGG	TCGTGAAAAT	1680
CAAAGGAAAT	TCCGTCATGT	GAGTGGAGGT	GCTGTAGTAG	GTGCTAGCAC	GAGGATGCCG	1740
GGTGGTGATA	CCTTGTCTCT	GGGTTTTGCT	CAGCTCTTTG	CGCGTGACAA	AGACTACTTT	1800
ATGAATACCA	ATTTTCGCAA	GACCTACGCA	GGATCTTTAC	GTTTGCAGCA	CGATGCTTCC	1860
CTATACTCTG	TGGTGAGTAT	CCTTTTAGGA	GAGGGAGGAC	TCCGCGAGAT	CCTGTTGCCT	1920
TATGTTTCCA	AGACTCTGCC	GTGCTCTTTC	TATGGGCAGC	TTAGCTACGG	CCATACGGAT	1980
CATCGCATGA	AGACCGAGTC	TCTACCCCCC	CCCCCCCCGA	CGCTCTCGAC	GGATCATACT	2040
TCTTGGGGAG	GATATGCTG	GGCTGGAGAG	CTGGGAACATC	GAGTTGCTGT	TGAAAATACC	2100
AGCGGCAGAG	GATTTTTCCG	AGAGTACACT	CCATTTGTAA	AAGTCCAAGC	TGTTTACTCG	2160
CGCCAAGATA	GCTTTGTTGA	ACTAGGAGCT	ATCAGTCGTG	ATTTTAGTGA	TTCGCATCTT	2220
TATAACCTTG	CGATTCTCTT	TGGAATCAAG	TTAGAGAAAC	GGTTTGCAGA	GCAATATTAT	2280
CATGTTGTAG	CGATGTATTC	TCCAGATGTT	TGTCGTAGTA	ACCCCAAATG	TACGACTACC	2340
CTACTTTCCA	ACCAAGGGAG	TTGGAAGACC	AAAGGTTCTGA	ACTTAGCAAG	ACAGGCTGGT	2400

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ATTGTTTCAGG CCTCAGGTTT TCGATCTTTG GGAGCTGCAG CAGAGCTTTT CGGGAACTTT 2460
GGCTTTGAAT GGCGGGGATC TTCTCGTAGC TATAATGTAG ATGCGGGTAG CAAAATCAAA 2520
TTTTAG 2526

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Lys Ile Pro Leu Arg Phe Leu Leu Ile Ser Leu Val Pro Thr Leu
 1             5             10             15
Ser Met Ser Asn Leu Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala
          20             25             30
Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys
          35             40             45
Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val
          50             55             60
Val Ile Glu Asn Val Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys
          65             70             75             80
Phe Lys Asn Asp Ala Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly
          85             90             95
Phe Ser Phe Thr Phe Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala
          100            105            110
Ala Ile Gly Ser Glu Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe
          115            120            125
Ser Ala Leu Ser Phe Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly
          130            135            140
Leu Gly Ala Ile Asn Val Lys Gly Asn Leu Ser Leu Leu Asp Asn Asp
          145            150            155            160
Lys Val Leu Ile Gln Asp Asn Phe Ser Thr Gly Asp Gly Gly Ala Ile
          165            170            175
Asn Cys Ala Gly Ser Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe
          180            185            190
Ile Gly Asn Ser Ser Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn
          195            200            205
Leu Thr Leu Ser Ser Gly Gly Glu Thr Leu Phe Gln Gly Asn Thr Ala
          210            215            220

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Pro Thr Ala Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly
 225 230 235 240
 Thr Leu Ser Ile Ser Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn
 245 250 255
 Thr Ile Gly Ala Thr Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly
 260 265 270
 Thr Ser Ala Lys Ile Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile
 275 280 285
 Tyr Phe Tyr Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp
 290 295 300
 Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr
 305 310 315 320
 Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys
 325 330 335
 Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys
 340 345 350
 Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly
 355 360 365
 Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser
 370 375 380
 Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn
 385 390 395 400
 Ile Asp Ser Leu Arg Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr
 405 410 415
 Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser
 420 425 430
 Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr
 435 440 445
 Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala
 450 455 460
 Asp Ser Arg Ser Ile Asn Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly
 465 470 475 480
 Lys Trp Thr Ile Asn Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser
 485 490 495
 Trp Ala Lys Gln Ser Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu
 500 505 510
 Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Pro Phe Gln
 515 520 525
 Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe

530	535	540
Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn 545 550 555 560		
Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser 565 570 575		
Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu 580 585 590		
Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr 595 600 605		
Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val 610 615 620		
Val Ser Ile Leu Leu Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro 625 630 635 640		
Tyr Val Ser Lys Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr 645 650 655		
Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro 660 665 670		
Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala 675 680 685		
Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly 690 695 700		
Phe Phe Arg Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ser 705 710 715 720		
Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser 725 730 735		
Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu 740 745 750		
Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro 755 760 765		
Asp Val Cys Arg Ser Asn Pro Lys Cys Thr Thr Thr Leu Leu Ser Asn 770 775 780		
Gln Gly Ser Trp Lys Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly 785 790 795 800		
Ile Val Gln Ala Ser Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu 805 810 815		
Phe Gly Asn Phe Gly Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn 820 825 830		
Val Asp Ala Gly Ser Lys Ile Lys Phe 835 840		

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2787 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAAGTCTT	CTTTCCCCAA	GTTTGTATTT	TCTACATTTG	CTATTTTCCC	TTTGTCTATG	60
ATTGCTACCG	AGACAGTTTT	GGATTCAAGT	GCGAGTTTCG	ATGGGAATAA	AAATGGTAAT	120
TTTTCAAGTTC	GTGAGAGTCA	GGAAGATGCT	GGAACCTACCT	ACCTATTTAA	GGGAAATGTC	180
ACTCTAGAAA	ATATTCTTGG	AACAGGCACA	GCAATCACAA	AAAGCTGTTT	TAACAACACT	240
AAGGGCGATT	TGACTTTTAC	AGGTAACGGG	AACTCTCTAT	TGTTCCAAAC	GGTGGATGCA	300
GGGACTGTAG	CAGGGGCTGC	TGTTAACAGC	AGCGTGGTAG	ATAAATCTAC	CACGTTTATA	360
GGGTTTTCTT	CGCTATCTTT	TATTGCGTCT	CCTGGAAGTT	CGATAACTAC	CGGCAAAGGA	420
GCCGTTAGCT	GCTCTACGGG	TAGCTTGAAG	TTTGACAAAA	ATGTCAGTTT	GCTCTTCAGC	480
AAAACTTTT	CAACGGATAA	TGGCGGTGCT	ATCACCPCAA	AAACTCTTTC	ATTAACAGGG	540
ACTACAATGT	CAGCTCTGTT	TTCTGAAAAAT	ACCTCCTCAA	AGAAAGGCGG	AGCCATTCAG	600
ACTTCCGATG	CCCTTACCAT	TACTGGAAAC	CAAGGGGAAG	TCTCTTTTTT	TGACAATACT	660
TCTTCGGATT	CTGGAGCTGC	AATTTTACAA	GAAGCCTCGG	TGACTATTTT	TAATAATGCT	720
AAAGTTTCCT	TTATTGACAA	TAAGGTCACA	GGAGCGAGCT	CCTCAACAAC	GGGGGATATG	780
TCAGGAGGTG	CTATCTGTGC	TTATAAAACT	AGTACAGATA	CTAAGGTCAC	CCTCACTGGA	840
AATCAGATGT	TACTCTTCAG	CAACAATACA	TCGACAACAG	CGGGAGGAGC	TATCTATGTG	900
AAAAAGCTCG	AACTGGCTTC	CGGAGGACTT	ACCCTATTCA	GTAGAAATAG	TGTCAATGGA	960
GGTACAGCTC	CTAAAGGTGG	AGCCATAGCT	ATCGAAGATA	GTGGGGAATT	GAGTTTATCC	1020
GCCGATAGTG	GTGACATTGT	CTTTTTAGGG	AATACAGTCA	CTTCTACTAC	TCCTGGGACG	1080
AATAGAAGTA	GTATCGACTT	AGGAACGAGT	GCAAAGATGA	CAGCTTTGCG	TTCTGCTGCT	1140
GGTAGAGCCA	TCTACTTCTA	TGATCCCAT	ACTACAGGAT	CTTCCACAAC	AGTTACAGAT	1200
GTCTTAAAG	TTAATGAGAC	TCCGGCAGAT	TCTGCACTAC	AATATACAGG	GAACATCATC	1260
TTCACAGGAG	AAAAGTTATC	AGAGACAGAG	GCCGCAGATT	CTAAAAATCT	TACTTCGAAG	1320
CTACTACAGC	CTGTAACCTT	TTCAGGAGGT	ACTCTATCTT	TAAAACATGG	AGTGACTCTG	1380
CAGACTCAGG	CATTCACTCA	ACAGGCAGAT	TCTCGTCTCG	AAATGGACGT	AGGAACTACT	1440
CTAGAACCTG	CTGATACTAG	CACCATAAAC	AATTTGGTCA	TTAACATCAG	TTCTATAGAC	1500
GGTGCAAAGA	AGGCAAAAAT	AGAAACCAAA	GCTACGTCAA	AAAATCTGAC	TTTATCTGGA	1560
ACCATCACTT	TATTGGACCC	GACGGGCACG	TTTTATGAAA	ATCATAGTTT	AAGAAATCCT	1620
CAGTCCTACG	ACATCTTAGA	GCTCAAAGCT	TCTGGAAGTG	TAACAAGCAC	CGCAGTGACT	1680
CCAGATCCTA	TAATGGGTGA	GAAATTCCAT	TACGGCTATC	AGGGAACTTG	GGGCCCCAAT	1740
GTTTGGGGGA	CAGGGGCTTC	TACGACTGCA	ACCTTCAACT	GGACTAAAAC	TGGCTATATT	1800
CCTAATCCCG	AGCGTATCGG	CTCTTTAGTC	CCTAATAGCT	TATGGAATGC	ATTTATAGAT	1860
ATTAGCTCTC	TCCATTATCT	TATGGAGACT	GCAAACGAAG	GGTTGCAGGG	AGACCGTGCT	1920
TTTTGGTGTG	CTGGATTATC	TAACCTCTTC	CATAAGGATA	GTACAAAAAC	ACGACGCGGG	1980
TTTCGCCATT	TGAGTGGCGG	TTATGTCATA	GGAGGAAACC	TACATACTTG	TTTCAAGATA	2040
ATTCTTAGTG	CTGCATTTTG	TCAGCTCTTT	GGAAGAGATA	GAGACTACTT	TGTAGCTAAG	2100
AATCAAGGTA	CAGTCTACGG	AGGAACTCTC	TATTACCAGC	ACAACGAAAC	CTATATCTCT	2160
CTTCCTTGCA	AACTACGGCC	TTGTTTCGTT	TCTTATGTTT	CTACAGAGAT	TCCTGTTCTC	2220
TTTTCAGGAA	ACCTTAGCTA	CACCCATACG	GATAACGATC	TGAAAACCAA	GTATACAACA	2280
TATCCTACTG	TTAAAGGAAG	CTGGGGGAAT	GATAGTTTCG	CTTTAGAATT	CGGTGGAAGA	2340
GCTCCGATTT	GCTTAGATGA	AAGTGCTCTA	TTTGAGCAGT	ACATGCCCTT	CATGAAATTG	2400
CAGTTTGTCT	ATGCACATCA	GGAAGGTTTT	AAAGAACAGG	GAACAGAAGC	TCGTGAATTT	2460
GGAAGTAGCC	GTCTTGTGAA	TCTTGCCTTA	CCTATCGGGA	TCCGATTGTA	TAAGGAATCA	2520
GACTGCCAAG	ATGCAACGTA	CAATCTAACT	CTTGGTTATA	CTGTGGATCT	TGTTTCGTAGT	2580
AACCCCGACT	GTACGACAAC	ACTGCGAATT	AGCGGTGATT	CTTGGAAAAC	CTTCGGTACG	2640
AATTTGGCAA	GACAAGCTTT	AGTCCTTCGT	GCAGGGAACC	ATTTTGTGCT	TAACCTCAAAT	2700

TTTGAAGCCT TTAGCCAATT TTCTTTTGAA TTGCGTGGGT CATCTCGCAA TTACAATGTA 2760
GACTTAGGAG CAAAATACCA ATTCTAA 2787

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met 1	Lys	Ser	Ser	Phe 5	Pro	Lys	Phe	Val	Phe 10	Ser	Thr	Phe	Ala	Ile 15	Phe
Pro	Leu	Ser	Met 20	Ile	Ala	Thr	Glu	Thr 25	Val	Leu	Asp	Ser	Ser 30	Ala	Ser
Phe	Asp	Gly 35	Asn	Lys	Asn	Gly	Asn 40	Phe	Ser	Val	Arg	Glu 45	Ser	Gln	Glu
Asp	Ala 50	Gly	Thr	Thr	Tyr	Leu 55	Phe	Lys	Gly	Asn	Val 60	Thr	Leu	Glu	Asn
Ile 65	Pro	Gly	Thr	Gly 70	Thr	Ala	Ile	Thr	Lys	Ser 75	Cys	Phe	Asn	Asn	Thr 80
Lys	Gly	Asp	Leu	Thr 85	Phe	Thr	Gly	Asn	Gly 90	Asn	Ser	Leu	Leu	Phe 95	Gln
Thr	Val	Asp	Ala 100	Gly	Thr	Val	Ala	Gly 105	Ala	Ala	Val	Asn	Ser 110	Ser	Val
Val	Asp	Lys 115	Ser	Thr	Thr	Phe	Ile 120	Gly	Phe	Ser	Ser 125	Leu	Ser	Phe	Ile
Ala	Ser 130	Pro	Gly	Ser	Ser	Ile 135	Thr	Thr	Gly	Lys	Gly 140	Ala	Val	Ser	Cys
Ser 145	Thr	Gly	Ser	Leu	Lys 150	Phe	Asp	Lys	Asn	Val 155	Ser	Leu	Leu	Phe	Ser 160
Lys	Asn	Phe	Ser	Thr 165	Asp	Asn	Gly	Gly	Ala 170	Ile	Thr	Ala	Lys	Thr 175	Leu
Ser	Leu	Thr	Gly 180	Thr	Thr	Met	Ser	Ala 185	Leu	Phe	Ser	Glu	Asn 190	Thr	Ser
Ser	Lys	Lys 195	Gly	Gly	Ala	Ile	Gln 200	Thr	Ser	Asp	Ala	Leu	Thr 205	Ile	Thr
Gly 210	Asn	Gln	Gly	Glu	Val	Ser 215	Phe	Ser	Asp	Asn	Thr 220	Ser	Ser	Asp	Ser
Gly	Ala	Ala	Ile	Phe	Thr	Glu	Ala	Ser	Val	Thr	Ile	Ser	Asn	Asn	Ala

225		230		235		240
Lys Val Ser Phe Ile Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr						
		245		250		255
Thr Gly Asp Met Ser Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr						
		260		265		270
Asp Thr Lys Val Thr Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn						
		275		280		285
Asn Thr Ser Thr Thr Ala Gly Gly Ala Ile Tyr Val Lys Lys Leu Glu						
		290		295		300
Leu Ala Ser Gly Gly Leu Thr Leu Phe Ser Arg Asn Ser Val Asn Gly						
		305		310		315
		320				
Gly Thr Ala Pro Lys Gly Gly Ala Ile Ala Ile Glu Asp Ser Gly Glu						
		325		330		335
Leu Ser Leu Ser Ala Asp Ser Gly Asp Ile Val Phe Leu Gly Asn Thr						
		340		345		350
Val Thr Ser Thr Thr Pro Gly Thr Asn Arg Ser Ser Ile Asp Leu Gly						
		355		360		365
Thr Ser Ala Lys Met Thr Ala Leu Arg Ser Ala Ala Gly Arg Ala Ile						
		370		375		380
Tyr Phe Tyr Asp Pro Ile Thr Thr Gly Ser Ser Thr Thr Val Thr Asp						
		385		390		395
		400				
Val Leu Lys Val Asn Glu Thr Pro Ala Asp Ser Ala Leu Gln Tyr Thr						
		405		410		415
Gly Asn Ile Ile Phe Thr Gly Glu Lys Leu Ser Glu Thr Glu Ala Ala						
		420		425		430
Asp Ser Lys Asn Leu Thr Ser Lys Leu Leu Gln Pro Val Thr Leu Ser						
		435		440		445
Gly Gly Thr Leu Ser Leu Lys His Gly Val Thr Leu Gln Thr Gln Ala						
		450		455		460
Phe Thr Gln Gln Ala Asp Ser Arg Leu Glu Met Asp Val Gly Thr Thr						
		465		470		475
		480				
Leu Glu Pro Ala Asp Thr Ser Thr Ile Asn Asn Leu Val Ile Asn Ile						
		485		490		495
Ser Ser Ile Asp Gly Ala Lys Lys Ala Lys Ile Glu Thr Lys Ala Thr						
		500		505		510
Ser Lys Asn Leu Thr Leu Ser Gly Thr Ile Thr Leu Leu Asp Pro Thr						
		515		520		525
Gly Thr Phe Tyr Glu Asn His Ser Leu Arg Asn Pro Gln Ser Tyr Asp						
		530		535		540

Ile	Leu	Glu	Leu	Lys	Ala	Ser	Gly	Thr	Val	Thr	Ser	Thr	Ala	Val	Thr	
545					550					555					560	
Pro	Asp	Pro	Ile	Met	Gly	Glu	Lys	Phe	His	Tyr	Gly	Tyr	Gln	Gly	Thr	
				565					570					575		
Trp	Gly	Pro	Ile	Val	Trp	Gly	Thr	Gly	Ala	Ser	Thr	Thr	Ala	Thr	Phe	
			580					585					590			
Asn	Trp	Thr	Lys	Thr	Gly	Tyr	Ile	Pro	Asn	Pro	Glu	Arg	Ile	Gly	Ser	
		595					600					605				
Leu	Val	Pro	Asn	Ser	Leu	Trp	Asn	Ala	Phe	Ile	Asp	Ile	Ser	Ser	Leu	
	610					615					620					
His	Tyr	Leu	Met	Glu	Thr	Ala	Asn	Glu	Gly	Leu	Gln	Gly	Asp	Arg	Ala	
625					630					635					640	
Phe	Trp	Cys	Ala	Gly	Leu	Ser	Asn	Phe	Phe	His	Lys	Asp	Ser	Thr	Lys	
				645					650					655		
Thr	Arg	Arg	Gly	Phe	Arg	His	Leu	Ser	Gly	Gly	Tyr	Val	Ile	Gly	Gly	
			660					665					670			
Asn	Leu	His	Thr	Cys	Ser	Asp	Lys	Ile	Leu	Ser	Ala	Ala	Phe	Cys	Gln	
		675					680					685				
Leu	Phe	Gly	Arg	Asp	Arg	Asp	Tyr	Phe	Val	Ala	Lys	Asn	Gln	Gly	Thr	
	690					695					700					
Val	Tyr	Gly	Gly	Thr	Leu	Tyr	Tyr	Gln	His	Asn	Glu	Thr	Tyr	Ile	Ser	
705					710					715				720		
Leu	Pro	Cys	Lys	Leu	Arg	Pro	Cys	Ser	Leu	Ser	Tyr	Val	Pro	Thr	Glu	
				725					730					735		
Ile	Pro	Val	Leu	Phe	Ser	Gly	Asn	Leu	Ser	Tyr	Thr	His	Thr	Asp	Asn	
			740					745					750			
Asp	Leu	Lys	Thr	Lys	Tyr	Thr	Thr	Tyr	Pro	Thr	Val	Lys	Gly	Ser	Trp	
		755					760					765				
Gly	Asn	Asp	Ser	Phe	Ala	Leu	Glu	Phe	Gly	Gly	Arg	Ala	Pro	Ile	Cys	
	770					775					780					
Leu	Asp	Glu	Ser	Ala	Leu	Phe	Glu	Gln	Tyr	Met	Pro	Phe	Met	Lys	Leu	
785					790					795					800	
Gln	Phe	Val	Tyr	Ala	His	Gln	Glu	Gly	Phe	Lys	Glu	Gln	Gly	Thr	Glu	
				805					810					815		
Ala	Arg	Glu	Phe	Gly	Ser	Ser	Arg	Leu	Val	Asn	Leu	Ala	Leu	Pro	Ile	
				820				825					830			
Gly	Ile	Arg	Phe	Asp	Lys	Glu	Ser	Asp	Cys	Gln	Asp	Ala	Thr	Tyr	Asn	
		835					840					845				

Leu Thr Leu Gly Tyr Thr Val Asp Leu Val Arg Ser Asn Pro Asp Cys
 850 855 860
 Thr Thr Thr Leu Arg Ile Ser Gly Asp Ser Trp Lys Thr Phe Gly Thr
 865 870 875 880
 Asn Leu Ala Arg Gln Ala Leu Val Leu Arg Ala Gly Asn His Phe Cys
 885 890 895
 Phe Asn Ser Asn Phe Glu Ala Phe Ser Gln Phe Ser Phe Glu Leu Arg
 900 905 910
 Gly Ser Ser Arg Asn Tyr Asn Val Asp Leu Gly Ala Lys Tyr Gln Phe
 915 920 925

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAGATCGT	CTTTTTCTT	GTTATTAATA	TCTTCATCTC	TAGCCTTTCC	TCTCTTAATG	60
AGTGTCTTCTG	CAGATGCTGC	CGATCTCACA	TTAGGGAGTC	GTGACAGTTA	TAATGGTGAT	120
ACAAGCACCA	CAGAATTTAC	TCCTAAAGCG	GCAACTTCTG	ATGCTAGTGG	CACGACCTAT	180
ATTCTCGATG	GGGATGTCTC	GATAAGCCAA	GCAGGGAAAC	AAACGAGCTT	AACCACAACT	240
TGTTTTTCTA	ACACTGCAGG	AAATCTTACC	TTCTTAGGGA	ACGGATTTTC	TCTTCATTTT	300
GACAAATATTA	TTTCGTCTAC	TGTTGCAGGT	GTTGTTGTTA	GCAATACAGC	AGCTTCTGGG	360
ATTACGAAAT	TCTCAGGATT	TTCAACTCTT	CGGATGCTTG	CAGCTCCTAG	GACCACAGGT	420
AAAGGAGCCA	TTAAAATTAC	CGATGGTCTG	GTGTTTGAGA	GTATAGGGAA	TCTTGACCAA	480
AATGAAAATG	CCTCTAGTGA	AAATGGGGGA	GCCATCAATA	CGAAGACTTT	GTCTTTGACT	540
GGGAGTACGC	GGTTTGTAGC	GTTCTTGTC	AATAGCTCGT	CGCAACAAGG	GGGAGCGATC	600
TATGCTTCTG	GTGACTCTGT	GATTTCTGAG	AATGCAGGAA	TCTTGAGCTT	CGGAAACAAC	660
AGTGCACAA	CATCAGGAGG	CGCGATCTCT	GCTGAAGGGA	ACCTTGTGAT	CTCCAATAAC	720
CAAAATATCT	TTTTCGATGG	CTGCAAAGCA	ACTACAAATG	GCGGAGCTAT	TGATTGTAAC	780
AAAGCAGGGG	CGAACCCAGA	CCCTATCTTG	ACTCTTTCAG	GAAATGAGAG	CCTGCATTTT	840
CTGAATAACA	CAGCAGGAAA	TAGTGGAGGT	GCGATTTATA	CCAAAAAATT	GGTGTATCC	900
TCAGGACGAG	GAGGAGTGTT	ATTTTCTAAC	AACAAAGCTG	CGAATGCTAC	TCCTAAAGGA	960
GGGGCAATTG	CGATTCTAGA	TTCTGGAGAG	ATTAGCATTT	CTGCAGATCT	CGGCAATATC	1020
ATTTTCGAGG	GCAATACTAC	GAGCACTACA	GGAAGTCCTG	CGAGTGTGAC	CAGAAATGCT	1080
ATAGATCTTG	CATCGAATGC	AAAATTTTTA	AATCTCCGAG	CGACTCGGGG	AAATAAAGTT	1140
ATTTTCTATG	ATCCTATCAC	GAGCTCAGGA	GCTACTGATA	AGCTCTCTTT	GAATAAAGCT	1200
GACGCAGGAT	CTGGAAATAC	CTATGAAGGC	TACATCGTTT	TCTCTGGAGA	GAAACTCTCA	1260
GAAGAGGAAC	TTAAGAAACC	TGACAATCTG	AAGTCTACAT	TTACACAGGC	TGTAGAGCTT	1320
GCTGCAGGTG	CCTTAGTATT	GAAAGATGGA	GTGACTGTAG	TTGCAAATAC	TATAACGCAG	1380
GTCGAGGGAT	CGAAAGTCGT	TATGGATGGA	GGGACTACTT	TTGAGGCAAG	CGCTGAGGGG	1440
GTCACCTCTA	ATGGCCTAGC	CATTAATATA	GATTCCTTAG	ATGGGACAAA	TAAAGCTATC	1500
ATTAAGGCCA	CGGCAGCAAG	TAAGGATGTT	GCCTTATCAG	GGCCTATCAT	GCTTGTAGAT	1560
GCTCAGGGGA	ACTATTATGA	GCATCATAAT	CTCAGTCAAC	AGCAGGTCTT	TCCTTTAATA	1620
GAGCTTTCTG	CACAAGGAAC	GATGACTACT	ACAGATATCC	CCGATACCCC	AATTCTAAAT	1680
ACTACGAATC	ACTATGGGTA	TCAAGGAACT	GGAATAATTG	TTTGGGTCGA	CGATGCAACT	1740
GCAAAAACAA	AAAATGCTAC	CTTAACCTTG	ACTAAAACAG	GATACAAGCC	GAATCCAGAA	1800
CGTCAGGGAC	CTTTGGTTCC	TAATAGCCTG	TGGGGTTCTT	TTGTGATGT	CCGCTCCATT	1860

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CAGAGCCTCA TGGACCGGAG CACAAGTTCG TTATCTTCGT CAACAAATTT GTGGGTATCA 1920
GGAATCGCGG ACTTTTTTGCA TGAAGATCAG AAAGGAAACC AACGTAGTTA TCGTCATTCT 1980
AGCGCGGGTT ATGCATTAGG AGGAGGATTC TTCACGGCTT CTGAAAATTT CTTTAATTTT 2040
GCTTTTTGTC AGCTTTTTTG CTACGACAAG GACCATCTTG TGGCTAAGAA CCATACCCAT 2100
GTATATGCAG GGGCAATGAG TTACCGACAC CTCGGAGAGT CTAAGACCCT CGCTAAGATT 2160
TTGTCAGGAA ATTCTGACTC CCTACCTTTT GTCTTCAATG CTCGGTTTGC TTATGGCCAT 2220
ACCGACAATA ACATGACCAC AAAGTACACT GGCTATTCTC CTGTTAAGGG AAGCTGGGGA 2280
AATGATGCCT TCGGTATAGA ATGTGGAGGA GCTATCCCGG TAGTTGCTTC AGGACGTCGG 2340
TCTTGGGTGG ATACCCACAC GCCATTCTA AACCTAGAGA TGATCTATGC ACATCAGAAT 2400
GACTTTAAGG AAAACGGCAC AGAAGGCCGT TCTTTCCAAA GTGAAGACCT CTTCAATCTA 2460
GCGGTTCTTG TAGGGATAAA ATTTGAGAAA TTCTCCGATA AGTCTACGTA TGATCTCTCC 2520
ATAGCTTACG TTCCCGATGT GATTCGTAAT GATCCAGGCT GCACGACAAC TCTTATGGTT 2580
TCTGGGGATT CTTGGTGCAC ATGTGGTACA AGCTTGTCTA GACAAGCTCT TCTTGTACGT 2640
GCTGGAAATC ATCATGCCTT TGCTTCAAAC TTTGAAGTTT TCAGTCAGTT TGAAGTCGAG 2700
TTGCGAGGTT CTTCTCGTAG CTATGCTATC GATCTTGGAG GAAGATTCGG ATTTTAA 2757

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Arg Ser Ser Phe Ser Leu Leu Leu Ile Ser Ser Ser Leu Ala Phe
 1             5             10             15

Pro Leu Leu Met Ser Val Ser Ala Asp Ala Ala Asp Leu Thr Leu Gly
 20             25             30

Ser Arg Asp Ser Tyr Asn Gly Asp Thr Ser Thr Thr Glu Phe Thr Pro
 35             40             45

Lys Ala Ala Thr Ser Asp Ala Ser Gly Thr Thr Tyr Ile Leu Asp Gly
 50             55             60

Asp Val Ser Ile Ser Gln Ala Gly Lys Gln Thr Ser Leu Thr Thr Ser
 65             70             75             80

Cys Phe Ser Asn Thr Ala Gly Asn Leu Thr Phe Leu Gly Asn Gly Phe
 85             90             95

Ser Leu His Phe Asp Asn Ile Ile Ser Ser Thr Val Ala Gly Val Val
100             105             110

Val Ser Asn Thr Ala Ala Ser Gly Ile Thr Lys Phe Ser Gly Phe Ser
115             120             125

Thr Leu Arg Met Leu Ala Ala Pro Arg Thr Thr Gly Lys Gly Ala Ile
130             135             140

Lys Ile Thr Asp Gly Leu Val Phe Glu Ser Ile Gly Asn Leu Asp Gln
145             150             155             160

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Asn Glu Asn Ala Ser Ser Glu Asn Gly Gly Ala Ile Asn Thr Lys Thr
 165 170 175
 Leu Ser Leu Thr Gly Ser Thr Arg Phe Val Ala Phe Leu Gly Asn Ser
 180 185 190
 Ser Ser Gln Gln Gly Gly Ala Ile Tyr Ala Ser Gly Asp Ser Val Ile
 195 200 205
 Ser Glu Asn Ala Gly Ile Leu Ser Phe Gly Asn Asn Ser Ala Thr Thr
 210 215 220
 Ser Gly Gly Ala Ile Ser Ala Glu Gly Asn Leu Val Ile Ser Asn Asn
 225 230 235 240
 Gln Asn Ile Phe Phe Asp Gly Cys Lys Ala Thr Thr Asn Gly Gly Ala
 245 250 255
 Ile Asp Cys Asn Lys Ala Gly Ala Asn Pro Asp Pro Ile Leu Thr Leu
 260 265 270
 Ser Gly Asn Glu Ser Leu His Phe Leu Asn Asn Thr Ala Gly Asn Ser
 275 280 285
 Gly Gly Ala Ile Tyr Thr Lys Lys Leu Val Leu Ser Ser Gly Arg Gly
 290 295 300
 Gly Val Leu Phe Ser Asn Asn Lys Ala Ala Asn Ala Thr Pro Lys Gly
 305 310 315 320
 Gly Ala Ile Ala Ile Leu Asp Ser Gly Glu Ile Ser Ile Ser Ala Asp
 325 330 335
 Leu Gly Asn Ile Ile Phe Glu Gly Asn Thr Thr Ser Thr Thr Gly Ser
 340 345 350
 Pro Ala Ser Val Thr Arg Asn Ala Ile Asp Leu Ala Ser Asn Ala Lys
 355 360 365
 Phe Leu Asn Leu Arg Ala Thr Arg Gly Asn Lys Val Ile Phe Tyr Asp
 370 375 380
 Pro Ile Thr Ser Ser Gly Ala Thr Asp Lys Leu Ser Leu Asn Lys Ala
 385 390 395 400
 Asp Ala Gly Ser Gly Asn Thr Tyr Glu Gly Tyr Ile Val Phe Ser Gly
 405 410 415
 Glu Lys Leu Ser Glu Glu Glu Leu Lys Lys Pro Asp Asn Leu Lys Ser
 420 425 430
 Thr Phe Thr Gln Ala Val Glu Leu Ala Ala Gly Ala Leu Val Leu Lys
 435 440 445
 Asp Gly Val Thr Val Val Ala Asn Thr Ile Thr Gln Val Glu Gly Ser
 450 455 460
 Lys Val Val Met Asp Gly Gly Thr Thr Phe Glu Ala Ser Ala Glu Gly

465		470		475		480
Val Thr Leu Asn Gly	Leu Ala Ile Asn Ile Asp Ser Leu Asp Gly Thr					
	485		490		495	
Asn Lys Ala Ile Ile Lys Ala Thr Ala Ala Ser Lys Asp Val Ala Leu						
	500		505		510	
Ser Gly Pro Ile Met Leu Val Asp Ala Gln Gly Asn Tyr Tyr Glu His						
	515		520		525	
His Asn Leu Ser Gln Gln Gln Val Phe Pro Leu Ile Glu Leu Ser Ala						
	530		535		540	
Gln Gly Thr Met Thr Thr Thr Asp Ile Pro Asp Thr Pro Ile Leu Asn						
	545		550		555	560
Thr Thr Asn His Tyr Gly Tyr Gln Gly Thr Gly Ile Ile Val Trp Val						
	565		570			575
Asp Asp Ala Thr Ala Lys Thr Lys Asn Ala Thr Leu Thr Trp Thr Lys						
	580		585		590	
Thr Gly Tyr Lys Pro Asn Pro Glu Arg Gln Gly Pro Leu Val Pro Asn						
	595		600		605	
Ser Leu Trp Gly Ser Phe Val Asp Val Arg Ser Ile Gln Ser Leu Met						
	610		615		620	
Asp Arg Ser Thr Ser Ser Leu Ser Ser Ser Thr Asn Leu Trp Val Ser						
	625		630		635	640
Gly Ile Ala Asp Phe Leu His Glu Asp Gln Lys Gly Asn Gln Arg Ser						
	645		650			655
Tyr Arg His Ser Ser Ala Gly Tyr Ala Leu Gly Gly Gly Phe Phe Thr						
	660		665		670	
Ala Ser Glu Asn Phe Phe Asn Phe Ala Phe Cys Gln Leu Phe Gly Tyr						
	675		680		685	
Asp Lys Asp His Leu Val Ala Lys Asn His Thr His Val Tyr Ala Gly						
	690		695		700	
Ala Met Ser Tyr Arg His Leu Gly Glu Ser Lys Thr Leu Ala Lys Ile						
	705		710		715	720
Leu Ser Gly Asn Ser Asp Ser Leu Pro Phe Val Phe Asn Ala Arg Phe						
	725		730		735	
Ala Tyr Gly His Thr Asp Asn Asn Met Thr Thr Lys Tyr Thr Gly Tyr						
	740		745		750	
Ser Pro Val Lys Gly Ser Trp Gly Asn Asp Ala Phe Gly Ile Glu Cys						
	755		760		765	
Gly Gly Ala Ile Pro Val Val Ala Ser Gly Arg Arg Ser Trp Val Asp						
	770		775		780	

Thr His Thr Pro Phe Leu Asn Leu Glu Met Ile Tyr Ala His Gln Asn
 785 790 795 800
 Asp Phe Lys Glu Asn Gly Thr Glu Gly Arg Ser Phe Gln Ser Glu Asp
 805 810 815
 Leu Phe Asn Leu Ala Val Pro Val Gly Ile Lys Phe Glu Lys Phe Ser
 820 825 830
 Asp Lys Ser Thr Tyr Asp Leu Ser Ile Ala Tyr Val Pro Asp Val Ile
 835 840 845
 Arg Asn Asp Pro Gly Cys Thr Thr Thr Leu Met Val Ser Gly Asp Ser
 850 855 860
 Trp Ser Thr Cys Gly Thr Ser Leu Ser Arg Gln Ala Leu Leu Val Arg
 865 870 875 880
 Ala Gly Asn His His Ala Phe Ala Ser Asn Phe Glu Val Phe Ser Gln
 885 890 895
 Phe Glu Val Glu Leu Arg Gly Ser Ser Arg Ser Tyr Ala Ile Asp Leu
 900 905 910
 Gly Gly Arg Phe Gly Phe
 915

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGAAATCCT	CTCTTCATTG	GTTTGTAATC	TCGTCATCTT	TAGCACTTCC	CTTGTCACTA	60
AATTTCTCTG	CGTTTGCTGC	TGTTGTTGAA	ATCAATCTAG	GACCTACCAA	TAGCTTCTCT	120
GGACCAGGAA	CCTACACTCC	TCCAGCCCAA	ACAACAAATG	CAGATGGAAC	TATCTATAAT	180
CTAACAGGGG	ATGTCTCAAT	CACCAATGCA	GGATCTCCGA	CAGCTCTAAC	CGCTTCCTGC	240
TTTAAAGAAA	CTACTGGGAA	TCTTTCTTTC	CAAGGCCACG	GCTACCAATT	TCTCCTACAA	300
AATATCGATG	CGGGAGCGAA	CTGTACCTTT	ACCAATACAG	CTGCAAATAA	GCTTCTCTCC	360
TTTTCAGGAT	TCTCCTATTT	GTCACTAATA	CAAACCACGA	ATGCTACCAC	AGGAACAGGA	420
GCCATCAAGT	CCACAGGAGC	TTGTTCTATT	CAGTCGAACT	ATAGTTGCTA	CTTTGGCCAA	480
AACTTTTCTA	ATGACAATGG	AGGCGCCCTC	CAAGGCAGCT	CTATCAGTCT	ATCGCTAAAC	540
CCCAACCTAA	CGTTTGCCAA	AAACAAAGCA	ACGCAAAAAG	GGGGTGCCCT	CTATTCCACG	600
GGAGGGATTA	CAATTAACAA	TACGTTAAAC	TCAGCATCAT	TTTCTGAAAA	TACCGCGGCG	660
AACAATGGCG	GAGCCATTTA	CACGGAAGCT	AGCAGTTTTA	TTAGCAGCAA	CAAAGCAATT	720
AGCTTTATAA	ACAATAGTGT	GACCGCAACC	TCAGCTACAG	GGGGAGCCAT	TTACTGTAGT	780
AGTACATCAG	CCCCCAAACC	AGTCTTAACT	CTATCAGACA	ACGGGGAAC	GAACCTTTATA	840
GGAAATACAG	CAATTACTAG	TGGTGGGGCG	ATTTATACTG	ACAATCTAGT	TCTTTCTTCT	900
GGAGGACCTA	CGCTTTTTTA	AAACAACTCT	GCTATAGATA	CTGCAGCTCC	CTTAGGAGGA	960
GCAATTGCGA	TTGCTGACTC	TGGATCTTTG	AGTCTTTCGG	CTCTTGGTGG	AGACATCACT	1020
TTTGAAGGAA	ACACAGTAGT	CAAAGGAGCT	TCTTCGAGTC	AGACCACTAC	CAGAAATTCT	1080

ATTAACATCG	GAAACACCAA	TGCTAAGATT	GTACAGCTGC	GAGCCTCTCA	AGGCAATACT	1140
ATCTACTTCT	ATGATCCTAT	AACAACCTAAC	CATACTGCAG	CTCTCTCAGA	TGCTCTAAAC	1200
TTAAATGGTC	CTGACCTTGC	AGGGAATCCT	GCATATCAAG	GAACCATCGT	ATTTTCTGGA	1260
GAGAAGCTCT	CGGAAGCAGA	AGCTGCAGAA	GCTGATAATC	TCAAATCTAC	AATTCAGCAA	1320
CCTCTAACTC	TTGCGGGAGG	GCAACTCTCT	CTTAAATCAG	GAGTCACTCT	AGTTGCTAAG	1380
TCCTTTTTCG	AATCTCCGGG	CTCTACCCCT	CTCATGGATG	CAGGGACCAC	ATTAGAAACC	1440
GCTGATGGGA	TCACTATCAA	TAATCTTGTT	CTCAATGTAG	ATTCTTTAAA	AGAGACCAAG	1500
AAGGCTACGC	TAAAGACAAC	ACAAGCAAGT	CAGACAGTCA	CTTTATCTGG	ATCGCTCTCT	1560
CTTGCTAGATC	CTTCTGGAAA	TGTCTACGAA	GATGTCTCTT	GGAATAACCC	TCAAGTCTTT	1620
TCTTGTCTCA	CTCTTACTGC	TGACGACCCC	GCGAATATTC	ACATCACAGA	CTTAGCTGCT	1680
GATCCCCTAG	AAAAAATCC	TATCCATTGG	GGATACCAAG	GGAATTGGGC	ATTATCTTGG	1740
CAAGAGGATA	CTGCGACTAA	ATCCAAAGCA	GCGACTCTTA	CCTGGACAAA	AACAGGATAC	1800
AATCCGAATC	CTGAGCGTCG	TGGAACCTTA	GTTGCTAACA	CGCTATGGGG	ATCCTTTGTT	1860
GATGTGCGCT	CCATACAACA	GCTTGTAGCC	ACTAAAGTAC	GCCAATCTCA	AGAAACTCGC	1920
GGCATCTGGT	GTGAAGGGAT	CTCGAACTTC	TTCCATAAAG	ATAGCACGAA	GATAAATAAA	1980
GGTTTTTCGCC	ACATAAGTGC	AGGTTATGTT	GTAGGAGCGA	CTACAACATT	AGCTTCTGAT	2040
AATCTTATCA	CTGACGCCTT	CTGCCAATTA	TTCCGGGAAA	ATAGAGATCA	CTTTATAAAT	2100
AAAAATAGAG	CTTCTGCCTA	TGCAGCTTCT	CTCCATCTCC	AGCATCTAGC	GACCTTGTCT	2160
TCTCCAAGCT	TGTTACGCTA	CCTTCCTGGA	TCTGAAAGTG	AGCAGCCTGT	CCTCTTTGAT	2220
GCTCAGATCA	GCTATATCTA	TAGTAAAAAT	ACTATGAAAA	CCTATTACAC	CCAAGCACCA	2280
AAGGGAGAGA	GCTCGTGGTA	TAATGACGGT	TGCGCTCTGG	AACTTGCGAG	CTCCCTACCA	2340
CACACTGCTT	TAAGCCATGA	GGGTCTCTTC	CACGCGTATT	TTCTTTTCAT	CAAAGTAGAA	2400
GCTTCGTACA	TACACCAAGA	TAGCTTCAAA	GAACGTAATA	CTACCTTGGT	ACGATCTTTC	2460
GATAGCGGTG	ATTTAATTAA	CGTCTCTGTG	CCTATTGGAA	TTACCTTCGA	GAGATTCTCG	2520
AGAAACGAGC	GTGCGTCTTA	CGAAGCTACT	GTCATCTACG	TTGCCGATGT	CTATCGTAAG	2580
AATCCTGACT	GCACGACAGC	TCTCCTAATC	AACAATACCT	CGTGGAACAC	TACAGGAACG	2640
AATCTCTCAA	GACAAGCTGG	TATCGGAAGA	GCAGGGATCT	TTTATGCCTT	CTCTCCAAAT	2700
CTTGAGGTCA	CAAGTAACCT	ATCTATGGAA	ATTCGTGGAT	CTTCACGCAG	CTACAATGCA	2760
GATCTTGGAG	GTAAGTTCCA	GTTCTAA				2787

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Ser	Ser	Leu	His	Trp	Phe	Val	Ile	Ser	Ser	Ser	Leu	Ala	Leu
1				5					10					15	
Pro	Leu	Ser	Leu	Asn	Phe	Ser	Ala	Phe	Ala	Ala	Val	Val	Glu	Ile	Asn
			20					25					30		
Leu	Gly	Pro	Thr	Asn	Ser	Phe	Ser	Gly	Pro	Gly	Thr	Tyr	Thr	Pro	Pro
			35					40					45		
Ala	Gln	Thr	Thr	Asn	Ala	Asp	Gly	Thr	Ile	Tyr	Asn	Leu	Thr	Gly	Asp
			50				55				60				
Val	Ser	Ile	Thr	Asn	Ala	Gly	Ser	Pro	Thr	Ala	Leu	Thr	Ala	Ser	Cys
			65				70				75				80
Phe	Lys	Glu	Thr	Thr	Gly	Asn	Leu	Ser	Phe	Gln	Gly	His	Gly	Tyr	Gln

85										90					95				
Phe	Leu	Leu	Gln	Asn	Ile	Asp	Ala	Gly	Ala	Asn	Cys	Thr	Phe	Thr	Asn				
			100					105					110						
Thr	Ala	Ala	Asn	Lys	Leu	Leu	Ser	Phe	Ser	Gly	Phe	Ser	Tyr	Leu	Ser				
		115					120					125							
Leu	Ile	Gln	Thr	Thr	Asn	Ala	Thr	Thr	Gly	Thr	Gly	Ala	Ile	Lys	Ser				
	130					135					140								
Thr	Gly	Ala	Cys	Ser	Ile	Gln	Ser	Asn	Tyr	Ser	Cys	Tyr	Phe	Gly	Gln				
145					150					155					160				
Asn	Phe	Ser	Asn	Asp	Asn	Gly	Gly	Ala	Leu	Gln	Gly	Ser	Ser	Ile	Ser				
				165					170					175					
Leu	Ser	Leu	Asn	Pro	Asn	Leu	Thr	Phe	Ala	Lys	Asn	Lys	Ala	Thr	Gln				
			180					185					190						
Lys	Gly	Gly	Ala	Leu	Tyr	Ser	Thr	Gly	Gly	Ile	Thr	Ile	Asn	Asn	Thr				
	195						200					205							
Leu	Asn	Ser	Ala	Ser	Phe	Ser	Glu	Asn	Thr	Ala	Ala	Asn	Asn	Gly	Gly				
	210					215					220								
Ala	Ile	Tyr	Thr	Glu	Ala	Ser	Ser	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Ile				
225					230					235					240				
Ser	Phe	Ile	Asn	Asn	Ser	Val	Thr	Ala	Thr	Ser	Ala	Thr	Gly	Gly	Ala				
			245					250						255					
Ile	Tyr	Cys	Ser	Ser	Thr	Ser	Ala	Pro	Lys	Pro	Val	Leu	Thr	Leu	Ser				
			260					265					270						
Asp	Asn	Gly	Glu	Leu	Asn	Phe	Ile	Gly	Asn	Thr	Ala	Ile	Thr	Ser	Gly				
		275					280					285							
Gly	Ala	Ile	Tyr	Thr	Asp	Asn	Leu	Val	Leu	Ser	Ser	Gly	Gly	Pro	Thr				
	290					295					300								
Leu	Phe	Lys	Asn	Asn	Ser	Ala	Ile	Asp	Thr	Ala	Ala	Pro	Leu	Gly	Gly				
305					310					315				320					
Ala	Ile	Ala	Ile	Ala	Asp	Ser	Gly	Ser	Leu	Ser	Leu	Ser	Ala	Leu	Gly				
				325				330						335					
Gly	Asp	Ile	Thr	Phe	Glu	Gly	Asn	Thr	Val	Val	Lys	Gly	Ala	Ser	Ser				
			340					345					350						
Ser	Gln	Thr	Thr	Thr	Arg	Asn	Ser	Ile	Asn	Ile	Gly	Asn	Thr	Asn	Ala				
			355				360					365							
Lys	Ile	Val	Gln	Leu	Arg	Ala	Ser	Gln	Gly	Asn	Thr	Ile	Tyr	Phe	Tyr				
	370					375					380								
Asp	Pro	Ile	Thr	Thr	Asn	His	Thr	Ala	Ala	Leu	Ser	Asp	Ala	Leu	Asn				
385					390					395					400				

Leu	Asn	Gly	Pro	Asp	Leu	Ala	Gly	Asn	Pro	Ala	Tyr	Gln	Gly	Thr	Ile	
				405					410						415	
Val	Phe	Ser	Gly	Glu	Lys	Leu	Ser	Glu	Ala	Glu	Ala	Ala	Glu	Ala	Asp	
			420					425					430			
Asn	Leu	Lys	Ser	Thr	Ile	Gln	Gln	Pro	Leu	Thr	Leu	Ala	Gly	Gly	Gln	
		435					440					445				
Leu	Ser	Leu	Lys	Ser	Gly	Val	Thr	Leu	Val	Ala	Lys	Ser	Phe	Ser	Gln	
	450					455					460					
Ser	Pro	Gly	Ser	Thr	Leu	Leu	Met	Asp	Ala	Gly	Thr	Thr	Leu	Glu	Thr	
465					470					475					480	
Ala	Asp	Gly	Ile	Thr	Ile	Asn	Asn	Leu	Val	Leu	Asn	Val	Asp	Ser	Leu	
				485					490						495	
Lys	Glu	Thr	Lys	Lys	Ala	Thr	Leu	Lys	Ala	Thr	Gln	Ala	Ser	Gln	Thr	
			500					505					510			
Val	Thr	Leu	Ser	Gly	Ser	Leu	Ser	Leu	Val	Asp	Pro	Ser	Gly	Asn	Val	
		515					520					525				
Tyr	Glu	Asp	Val	Ser	Trp	Asn	Asn	Pro	Gln	Val	Phe	Ser	Cys	Leu	Thr	
	530					535					540					
Leu	Thr	Ala	Asp	Asp	Pro	Ala	Asn	Ile	His	Ile	Thr	Asp	Leu	Ala	Ala	
545					550					555					560	
Asp	Pro	Leu	Glu	Lys	Asn	Pro	Ile	His	Trp	Gly	Tyr	Gln	Gly	Asn	Trp	
				565					570					575		
Ala	Leu	Ser	Trp	Gln	Glu	Asp	Thr	Ala	Thr	Lys	Ser	Lys	Ala	Ala	Thr	
			580					585					590			
Leu	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Asn	Pro	Glu	Arg	Arg	Gly	
		595				600						605				
Thr	Leu	Val	Ala	Asn	Thr	Leu	Trp	Gly	Ser	Phe	Val	Asp	Val	Arg	Ser	
	610					615					620					
Ile	Gln	Gln	Leu	Val	Ala	Thr	Lys	Val	Arg	Gln	Ser	Gln	Glu	Thr	Arg	
625					630					635					640	
Gly	Ile	Trp	Cys	Glu	Gly	Ile	Ser	Asn	Phe	Phe	His	Lys	Asp	Ser	Thr	
				645					650					655		
Lys	Ile	Asn	Lys	Gly	Phe	Arg	His	Ile	Ser	Ala	Gly	Tyr	Val	Val	Gly	
		660						665					670			
Ala	Thr	Thr	Thr	Leu	Ala	Ser	Asp	Asn	Leu	Ile	Thr	Ala	Ala	Phe	Cys	
		675					680					685				
Gln	Leu	Phe	Gly	Lys	Asp	Arg	Asp	His	Phe	Ile	Asn	Lys	Asn	Arg	Ala	
	690					695					700					

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Ser Ala Tyr Ala Ala Ser Leu His Leu Gln His Leu Ala Thr Leu Ser
705                      710                      715                      720

Ser Pro Ser Leu Leu Arg Tyr Leu Pro Gly Ser Glu Ser Glu Gln Pro
                      725                      730                      735

Val Leu Phe Asp Ala Gln Ile Ser Tyr Ile Tyr Ser Lys Asn Thr Met
                      740                      745                      750
Lys Thr Tyr Tyr Thr Gln Ala Pro Lys Gly Glu Ser Ser Trp Tyr Asn
                      755                      760                      765

Asp Gly Cys Ala Leu Glu Leu Ala Ser Ser Leu Pro His Thr Ala Leu
770                      775                      780

Ser His Glu Gly Leu Phe His Ala Tyr Phe Pro Phe Ile Lys Val Glu
785                      790                      795                      800

Ala Ser Tyr Ile His Gln Asp Ser Phe Lys Glu Arg Asn Thr Thr Leu
                      805                      810                      815

Val Arg Ser Phe Asp Ser Gly Asp Leu Ile Asn Val Ser Val Pro Ile
                      820                      825                      830

Gly Ile Thr Phe Glu Arg Phe Ser Arg Asn Glu Arg Ala Ser Tyr Glu
                      835                      840                      845

Ala Thr Val Ile Tyr Val Ala Asp Val Tyr Arg Lys Asn Pro Asp Cys
850                      855                      860

Thr Thr Ala Leu Leu Ile Asn Asn Thr Ser Trp Lys Thr Thr Gly Thr
865                      870                      875                      880

Asn Leu Ser Arg Gln Ala Gly Ile Gly Arg Ala Gly Ile Phe Tyr Ala
                      885                      890                      895

Phe Ser Pro Asn Leu Glu Val Thr Ser Asn Leu Ser Met Glu Ile Arg
                      900                      905                      910

Gly Ser Ser Arg Ser Tyr Asn Ala Asp Leu Gly Gly Lys Phe Gln Phe
915                      920                      925

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

ATGAAAATAC CCTTGACAA ACTCCTGATC TCTTCGACTC TTGTCCTCC CATTCTATTG      60
AGCATTGCAA CTTACGGAGC AGATGCTTCT TTATCCCCTA CAGATAGCTT TGATGGAGCG      120
GGCGGCTCTA CATTCTACTCC AAAATCTACA GCAGATGCCA ATGGAACGAA CTATGTCTTA      180
TCAGGAAATG TCTATATAAA CGATGCTGGG AAAGGCACAG CATTAAACAGG CTGCTGCTTT      240
ACAGAAACTA CGGGTGATCT GACATTTACT GGAAAGGGAT ACTCATTTTC ATTCAACACG      300

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GTAGATGCGG	GTTCTGAATGC	AGGAGCTGCG	GCAAGCACAA	CTGCTGATAA	AGCCCTAACA	360
TTCACAGGAT	TTTCTAACCT	TTCCTTCATT	GCAGCTCCTG	GAAGTACAGT	TGCTTCAGGA	420
AAAAGTACTT	TAAGTTCTGC	AGGAGCCTTA	AATCTTACCG	ATAATGGAAC	GATTCTCTTT	480
AGCCAAAACG	TCTCCAATGA	AGCTAATAAC	AATGGCGGAG	CGATCACCAC	AAAACTCTT	540
TCTATTTCTG	GGAATACCTC	TTCTATAACC	TTCAGTAGTA	ATAGCGCAA	AAAATTAGGT	600
GGAGCGATCT	ATAGCTCTGC	GGCTGCAAGT	ATTTTCAGGAA	ACACCGGCCA	GTTAGTCTTT	660
ATGAATAATA	AAGGAGAAAC	TGGGGGCGGG	GCTCTGGGCT	TTGAAGCCAG	CTCCTCGATT	720
ACTCAAAATA	GTCCTCTTTT	CTTCTCTGGA	AACACTGCAA	CAGATGCTGC	AGGCAAGGGC	780
GGGGCCATTT	ATTGTGAAAA	AACAGGAGAG	ACTCCTACTC	TTACTATCTC	TGGAAATAAA	840
AGTCTGACCT	TCGCCGAGAA	CTCTTCAGTA	ACTCAAGGCG	GAGCAATCTG	TGCCCATGGT	900
CTAGATCTTT	CCGCTGCTGG	CCCTACCCTA	TTTTCAAATA	ATAGATGCGG	GAACACAGCT	960
GCAGGCAAGG	GCGGCGCTAT	TGCAATTGCC	GACTCTGGAT	CTTTAAGTCT	CTCTGCAAAT	1020
CAAGGAGACA	TCACGTTCCCT	TGGCAACACT	CTAACCTCAA	CCTCCGCGCC	AACATCGACA	1080
CGGAATGCTA	TCTACCTGGG	ATCGTCAGCA	AAAATTACGA	ACTTAAGGGC	AGCCCAAGGC	1140
CAATCTATCT	ATTTCTATGA	TCCGATTGCA	TCTAACACCA	CAGGAGCTTC	AGACGTTCTG	1200
ACCATCAACC	AACCGGATAG	CAACTCGCCT	TTAGATTATT	CAGGAACGAT	TGTATTTTCT	1260
GGGGAAAAGC	TCTCTGCAGA	TGAAGCGAAA	GCTGCTGATA	ACTTCACATC	TATATTAAAG	1320
CAACCATTTG	CTCTAGCCTC	TGGAACCTTA	GCACTCAAAG	GAAATGTCTG	GTTAGATGTC	1380
AATGGTTTCA	CACAGACTGA	AGGCTCTACA	CTCCTCATGC	AACCAGGAAC	AAAGCTCAAA	1440
GCAGATACTG	AAGCTATCAG	TCTTACCAAA	CTTGTCGTTG	ATCTTTCTGC	CTTAGAGGGA	1500
AATAAGAGTG	TGTCCATTGA	AACAGCAGGA	GCCAACAAAA	CTATAACTCT	AACCTCTCCT	1560
CTTGTTTTCC	AAGATAGTAG	CGGCAATTTT	TATGAAAGCC	ATACGATAAA	CCAAGCCTTC	1620
ACGCAGCCTT	TGGTGGTATT	CACTGCTGCT	ACTGCTGCTA	GCGATATTTA	TATCGATGCG	1680
CTTCTCACTT	CTCCAGTACA	AACTCCAGAA	CCTCATTACG	GGTATCAGGG	ACATTGGGAA	1740
GCCACTTGGG	CAGACACATC	AACTGCAAAA	TCAGGAACTA	TGACTTGGGT	AACTACGGGC	1800
TACAACCCTA	ATCCTGAGCG	TAGAGCTTCC	GTAGTTCCCG	ATTCATTATG	GGCATCCTTT	1860
ACTGACATTC	GCACTCTACA	GCAGATCATG	ACATCTCAAG	CGAATAGTAT	CTATCAGCAA	1920
CGAGGACTCT	GGGCATCAGG	AACTGCGAAT	TTCTTCCATA	AGGATAAATC	AGGAACAAAC	1980
CAAGCATTCC	GACATAAAAG	CTACGGCTAT	ATTGTTGGAG	GAAGTGCTGA	AGATTTTCT	2040
GAAAATATCT	TCAGTGTAGC	TTTCTGCCAG	CTCTTCGGTA	AAGATAAAGA	CCTGTTTATA	2100
GTTGAAAATA	CCTCTCATAA	CTATTTAGCG	TCGCTATACC	TGCAACATCG	AGCATTCCTA	2160
GGAGGACTTC	CCATGCCCTC	ATTTGGAAGT	ATCACCGACA	TGCTGAAAGA	TATTCCTCTC	2220
ATTTTGAATG	CCCAGCTAAG	CTACAGCTAC	ACTAAAAATG	ATATGGATAC	TCGCTATACT	2280
TCCTATCCTG	AAGCTCAAGG	TTCTTGGACC	AATAATTCTG	GGGCTCTAGA	GCTCGGAGGA	2340
TCTCTGGCTC	TATATCTCCC	TAAAGAAGCA	CCGTTCTTCC	AGGGATATTT	CCCCTTCTTA	2400
AAGTTCCAGG	CAGTCTACAG	CCGCCAACAA	AACTTTAAAG	AGAGTGGCGC	TGAAGCCCGT	2460
GCTTTTGATG	ATGGAGACCT	AGTGAAGTGC	TCTATCCCTG	TCGGCATTCT	GTTAGAAAAA	2520
ATCTCCGAAG	ATGAAAAAAA	TAATTTTCGAG	ATTTCTCTAG	CCAACATTGG	TGATGTGTAT	2580
CGTAAAAATC	CCGTTTCGCG	TACTTCTCTA	ATGGTCAGTG	GAGCCTCTTG	GACTTCGCTA	2640
TGTAAAAACC	TCGCACGACA	AGCCTTCTTA	GCAAGTGCTG	GAAGCCATCT	GACTCTCTCC	2700
CCTCATGTAG	AACTCTCTGG	GGAAGCTGCT	TATGAGCTTC	GTGGCTCAGC	ACACATCTAC	2760
AATGTAGATT	GTGGGCTAAG	ATACTCATTC	TAG			2793

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Lys	Ile	Pro	Leu	His	Lys	Leu	Leu	Ile	Ser	Ser	Thr	Leu	Val	Thr
1							5								15
									10						

Pro Ile Leu Leu Ser Ile Ala Thr Tyr Gly Ala Asp Ala Ser Leu Ser
 20 25 30

Pro Thr Asp Ser Phe Asp Gly Ala Gly Gly Ser Thr Phe Thr Pro Lys
 35 40 45

Ser Thr Ala Asp Ala Asn Gly Thr Asn Tyr Val Leu Ser Gly Asn Val
 50 55 60

Tyr Ile Asn Asp Ala Gly Lys Gly Thr Ala Leu Thr Gly Cys Cys Phe
 65 70 75 80

Thr Glu Thr Thr Gly Asp Leu Thr Phe Thr Gly Lys Gly Tyr Ser Phe
 85 90 95

Ser Phe Asn Thr Val Asp Ala Gly Ser Asn Ala Gly Ala Ala Ala Ser
 100 105 110

Thr Thr Ala Asp Lys Ala Leu Thr Phe Thr Gly Phe Ser Asn Leu Ser
 115 120 125

Phe Ile Ala Ala Pro Gly Thr Thr Val Ala Ser Gly Lys Ser Thr Leu
 130 135 140

Ser Ser Ala Gly Ala Leu Asn Leu Thr Asp Asn Gly Thr Ile Leu Phe
 145 150 155 160

Ser Gln Asn Val Ser Asn Glu Ala Asn Asn Asn Gly Gly Ala Ile Thr
 165 170 175

Thr Lys Thr Leu Ser Ile Ser Gly Asn Thr Ser Ser Ile Thr Phe Thr
 180 185 190

Ser Asn Ser Ala Lys Lys Leu Gly Gly Ala Ile Tyr Ser Ser Ala Ala
 195 200 205

Ala Ser Ile Ser Gly Asn Thr Gly Gln Leu Val Phe Met Asn Asn Lys
 210 215 220

Gly Glu Thr Gly Gly Gly Ala Leu Gly Phe Glu Ala Ser Ser Ser Ile
 225 230 235 240

Thr Gln Asn Ser Ser Leu Phe Phe Ser Gly Asn Thr Ala Thr Asp Ala
 245 250 255

Ala Gly Lys Gly Gly Ala Ile Tyr Cys Glu Lys Thr Gly Glu Thr Pro
 260 265 270

Thr Leu Thr Ile Ser Gly Asn Lys Ser Leu Thr Phe Ala Glu Asn Ser
 275 280 285

Ser Val Thr Gln Gly Gly Ala Ile Cys Ala His Gly Leu Asp Leu Ser
 290 295 300

Ala Ala Gly Pro Thr Leu Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala
 305 310 315 320

Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser
 325 330 335

Leu Ser Ala Asn Gln Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr
 340 345 350
 Ser Thr Ser Ala Pro Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser
 355 360 365
 Ser Ala Lys Ile Thr Asn Leu Arg Ala Ala Gln Gly Gln Ser Ile Tyr
 370 375 380
 Phe Tyr Asp Pro Ile Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu
 385 390 395 400
 Thr Ile Asn Gln Pro Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr
 405 410 415
 Ile Val Phe Ser Gly Glu Lys Leu Ser Ala Asp Glu Ala Lys Ala Ala
 420 425 430
 Asp Asn Phe Thr Ser Ile Leu Lys Gln Pro Leu Ala Leu Ala Ser Gly
 435 440 445
 Thr Leu Ala Leu Lys Gly Asn Val Glu Leu Asp Val Asn Gly Phe Thr
 450 455 460
 Gln Thr Glu Gly Ser Thr Leu Leu Met Gln Pro Gly Thr Lys Leu Lys
 465 470 475 480
 Ala Asp Thr Glu Ala Ile Ser Leu Thr Lys Leu Val Val Asp Leu Ser
 485 490 495
 Ala Leu Glu Gly Asn Lys Ser Val Ser Ile Glu Thr Ala Gly Ala Asn
 500 505 510
 Lys Thr Ile Thr Leu Thr Ser Pro Leu Val Phe Gln Asp Ser Ser Gly
 515 520 525
 Asn Phe Tyr Glu Ser His Thr Ile Asn Gln Ala Phe Thr Gln Pro Leu
 530 535 540
 Val Val Phe Thr Ala Ala Thr Ala Ala Ser Asp Ile Tyr Ile Asp Ala
 545 550 555 560
 Leu Leu Thr Ser Pro Val Gln Thr Pro Glu Pro His Tyr Gly Tyr Gln
 565 570 575
 Gly His Trp Glu Ala Thr Trp Ala Asp Thr Ser Thr Ala Lys Ser Gly
 580 585 590
 Thr Met Thr Trp Val Thr Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg
 595 600 605
 Ala Ser Val Val Pro Asp Ser Leu Trp Ala Ser Phe Thr Asp Ile Arg
 610 615 620
 Thr Leu Gln Gln Ile Met Thr Ser Gln Ala Asn Ser Ile Tyr Gln Gln
 625 630 635 640

Arg Gly Leu Trp Ala Ser Gly Thr Ala Asn Phe Phe His Lys Asp Lys
 645 650 655
 Ser Gly Thr Asn Gln Ala Phe Arg His Lys Ser Tyr Gly Tyr Ile Val
 660 665 670
 Gly Gly Ser Ala Glu Asp Phe Ser Glu Asn Ile Phe Ser Val Ala Phe
 675 680 685
 Cys Gln Leu Phe Gly Lys Asp Lys Asp Leu Phe Ile Val Glu Asn Thr
 690 695 700
 Ser His Asn Tyr Leu Ala Ser Leu Tyr Leu Gln His Arg Ala Phe Leu
 705 710 715 720
 Gly Gly Leu Pro Met Pro Ser Phe Gly Ser Ile Thr Asp Met Leu Lys
 725 730 735
 Asp Ile Pro Leu Ile Leu Asn Ala Gln Leu Ser Tyr Ser Tyr Thr Lys
 740 745 750
 Asn Asp Met Asp Thr Arg Tyr Thr Ser Tyr Pro Glu Ala Gln Gly Ser
 755 760 765
 Trp Thr Asn Asn Ser Gly Ala Leu Glu Leu Gly Gly Ser Leu Ala Leu
 770 775 780
 Tyr Leu Pro Lys Glu Ala Pro Phe Phe Gln Gly Tyr Phe Pro Phe Leu
 785 790 795 800
 Lys Phe Gln Ala Val Tyr Ser Arg Gln Gln Asn Phe Lys Glu Ser Gly
 805 810 815
 Ala Glu Ala Arg Ala Phe Asp Asp Gly Asp Leu Val Asn Cys Ser Ile
 820 825 830
 Pro Val Gly Ile Arg Leu Glu Lys Ile Ser Glu Asp Glu Lys Asn Asn
 835 840 845
 Phe Glu Ile Ser Leu Ala Asn Ile Gly Asp Val Tyr Arg Lys Asn Pro
 850 855 860
 Arg Ser Arg Thr Ser Leu Met Val Ser Gly Ala Ser Trp Thr Ser Leu
 865 870 875 880
 Cys Lys Asn Leu Ala Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His
 885 890 895
 Leu Thr Leu Ser Pro His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu
 900 905 910
 Leu Arg Gly Ser Ala His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr
 915 920 925
 Ser Phe
 930

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
GAAGACAATA TAAGGTACCG TCATAACAGC GGGGGTTATG CACTAGGGAT CACAGCAACA      60
ACTCCTGCCG AGGATCAGCT TACTTTTGCC TTCTGCCAGC TCTTTGCTAG AGATCGCAAT     120
CATATTACAG GTAAGAACCA CGGAGATACT TACGGTGCCT CTTTGTATTT CCACCATACA     180
GAAGGGCTCT TCGACATCGC CAATTTCTCT TGGGGAAAAG CAACCCGAGC TCCCTGGGTG     240
CTCTCTGAGA TCTCCCAGAT CATTCCCTTA TCGTTCGATG CTAAATTCAG TTATCTCCAT     300
ACAGACAACC ACATGAAGAC ATATTATACC GATAACTCTA TCATCAAGGG TTCTTGGAGA     360
AACGATGCCT TCTGTGCAGA TCTTGGAGCT AGCCTGCCTT TTGTTATTTT CGTTCCGTAT     420
CTTCTGAAAG AAGTCGAACC TTTTGTCAAA GTACAGTATA TCTATGCGCA TCAGCAAGAC     480
TTCTACGAGC GTCATGCTGA AGGACGCGCT TTCAATAAAA GCGAGCTTAT CAACGTAGAG     540
ATTCCTATAG GCGTCACCTT CGAAAGAGAC TCAAAATCAG AAAAGGGAAC TTACGATCTT     600
ACTCTTATGT ATATACTCGA TGCTTACCGA CGCAATCCTA AATGTCAAAC TTCCCTAATA     660
GCTAGCGATG CTAAGTGGAT GGCCTATGGT ACCAACCTCG CACGACAAGG FTTTTCTGTT     720
CGTGCTGCGA ACCATTTCCA AGTGAACCCC CACATGGAAA TCTTCGGTCA ATTCGCTTTT     780
GAAGTACGAA GTTCTTCACG AAATTATAAT ACAAACCTAG GCTCTAAGTT TTGTTTCTAG     840
```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Ala Leu Gly
 1              5              10              15

Ile Thr Ala Thr Thr Pro Ala Glu Asp Gln Leu Thr Phe Ala Phe Cys
      20              25              30

Gln Leu Phe Ala Arg Asp Arg Asn His Ile Thr Gly Lys Asn His Gly
      35              40              45

Asp Thr Tyr Gly Ala Ser Leu Tyr Phe His His Thr Glu Gly Leu Phe
      50              55              60

Asp Ile Ala Asn Phe Leu Trp Gly Lys Ala Thr Arg Ala Pro Trp Val
      65              70              75              80

Leu Ser Glu Ile Ser Gln Ile Ile Pro Leu Ser Phe Asp Ala Lys Phe
      85              90              95

Ser Tyr Leu His Thr Asp Asn His Met Lys Thr Tyr Tyr Thr Asp Asn
      100              105              110
```

Ser Ile Ile Lys Gly Ser Trp Arg Asn Asp Ala Phe Cys Ala Asp Leu
 115 120 125
 Gly Ala Ser Leu Pro Phe Val Ile Ser Val Pro Tyr Leu Leu Lys Glu
 130 135 140
 Val Glu Pro Phe Val Lys Val Gln Tyr Ile Tyr Ala His Gln Gln Asp
 145 150 155 160
 Phe Tyr Glu Arg His Ala Glu Gly Arg Ala Phe Asn Lys Ser Glu Leu
 165 170 175
 Ile Asn Val Glu Ile Pro Ile Gly Val Thr Phe Glu Arg Asp Ser Lys
 180 185 190
 Ser Glu Lys Gly Thr Tyr Asp Leu Thr Leu Met Tyr Ile Leu Asp Ala
 195 200 205
 Tyr Arg Arg Asn Pro Lys Cys Gln Thr Ser Leu Ile Ala Ser Asp Ala
 210 215 220
 Asn Trp Met Ala Tyr Gly Thr Asn Leu Ala Arg Gln Gly Phe Ser Val
 225 230 235 240
 Arg Ala Ala Asn His Phe Gln Val Asn Pro His Met Glu Ile Phe Gly
 245 250 255
 Gln Phe Ala Phe Glu Val Arg Ser Ser Ser Arg Asn Tyr Asn Thr Asn
 260 265 270
 Leu Gly Ser Lys Phe Cys Phe
 275

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGACCATAC	TTCGAAATTT	TCTTACCTGC	TCGGCTTTAT	TCCTCGCTCT	CCCTGCAGCA	60
GCACAAGTTG	TATATCTTCA	TGAAAGTGAT	GGTTATAACG	GTGCTATCAA	TAATAAAAGC	120
TTAGAACCTA	AAATTACCTG	TTATCCAGAA	GGAACCTTCT	ACATCTTTCT	AGATGACGTG	180
AGGATTTCCA	ACGTTAAGCA	TGATCAAGAA	GATGCTGGGG	TTTTTATAAA	TCGATCTGGG	240
AATCTTTTTT	TCATGGGCAA	CCGTTGCAAC	TTCACTTTTT	ACAACCTTAT	GACCGAGGGT	300
TTTGGCGCTG	CCATTTTCGAA	CCGCGTTGGA	GACACCACTC	TCACTCTCTC	TAATTTTCTT	360
TACTTAACGT	TCACCTCAGC	ACCTCTACTA	CCTCAAGGAC	AAGGAGCGAT	TTATAGTCTT	420
GGTTCGCTGA	TGATCGAAAA	TAGTGAGGAA	GTGACTTTCT	GTGGGAACTA	CTCTTCGTGG	480
AGTGGAGCTG	CGATTTTATAC	TCCCTACCTT	TTAGGTTCTA	AGGCGAGTCG	TCCTTCAGTA	540
AATCTCAGCG	GGAACCGCTA	CCTGGTGTTT	AGAGACTATG	TGAGCCAAGG	TTATGGCGGC	600
GCCGTATCTA	CCCACAATCT	CACACTCACG	ACTCGAGGAC	CTTCGTGTTT	TGAAAATAAT	660
CATGCTTATC	ATGACGTGAA	TAGTAATGGA	GGAGCCATTG	CCATTGCTCC	TGGAGGATCG	720

ATCTCTATAT	CCGTGAAAAG	CGGAGATCTC	ATCTTCAAAG	GAAATACAGC	ATCACAAGAC	780
GGAAATACAA	TACACAACCTC	CATCCATCTG	CAATCTGGAG	CACAGTTTAA	GAACCTACGT	840
GCTGTTTCAG	AATCCGGAGT	TTATTTCTAT	GATCCTATAA	GCCATAGCGA	GTCGCATAAA	900
ATTACAGATC	TTGTAATCAA	TGCTCCTGAA	GGAAAGGAAA	CTTATGAAGG	AACAATTAGC	960
TTCTCAGGAC	TATGCCTGGA	TGATCATGAA	GTTTGTGCGG	AAAATCTTAC	TTCCACAATC	1020
CTACAAGATG	TCACATTAGC	AGGAGGAACT	CTCTCTCTAT	CGGATGGGGT	TACCTTGCAA	1080
CTGCATTCTT	TTAAGCAGGA	AGCAAGCTCT	ACGCTTACTA	TGTCTCCAGG	AACCACTCTG	1140
CTCTGCTCAG	GAGATGCTCG	GGTTCAGAAT	CTGCACATCC	TGATTGAAGA	TACCGACAAC	1200
TTTGTTCCCTG	TAAGGATTCG	CGCCGAGGAC	AAGGATGCTC	TTGTCTCATT	AGAAAACTT	1260
AAAGTTGCCT	TTGAGGCTTA	TTGGTCCGTC	TATGACTTTC	CTCAATTTAA	GGAAGCCTTT	1320
ACGATTCCCTC	TTCTTGAAC	TCTAGGGCCT	TCTTTTGACA	GTCTTCTCCT	AGGGGAGACC	1380
ACTTTGGAGA	GAACCCAAGT	CACAACAGAG	AATGACGCCG	TTCGAGGTTT	CTGGTCCCTA	1440
AGCTGGGAAG	AGTACCCCC	TTCTCTGGAT	AAAGACAGAA	GGATCACACC	AACTAAGAAA	1500
ACTGTTTTCC	TCACTTGGA	TCCTGAGATC	ACTTCTACGC	CATAA		1545

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Thr	Ile	Leu	Arg	Asn	Phe	Leu	Thr	Cys	Ser	Ala	Leu	Phe	Leu	Ala	1	5	10	15
Leu	Pro	Ala	Ala	Ala	Gln	Val	Val	Tyr	Leu	His	Glu	Ser	Asp	Gly	Tyr	20	25	30	
Asn	Gly	Ala	Ile	Asn	Asn	Lys	Ser	Leu	Glu	Pro	Lys	Ile	Thr	Cys	Tyr	35	40	45	
Pro	Glu	Gly	Thr	Ser	Tyr	Ile	Phe	Leu	Asp	Asp	Val	Arg	Ile	Ser	Asn	50	55	60	
Val	Lys	His	Asp	Gln	Glu	Asp	Ala	Gly	Val	Phe	Ile	Asn	Arg	Ser	Gly	65	70	75	80
Asn	Leu	Phe	Phe	Met	Gly	Asn	Arg	Cys	Asn	Phe	Thr	Phe	His	Asn	Leu	85	90	95	
Met	Thr	Glu	Gly	Phe	Gly	Ala	Ala	Ile	Ser	Asn	Arg	Val	Gly	Asp	Thr	100	105	110	
Thr	Leu	Thr	Leu	Ser	Asn	Phe	Ser	Tyr	Leu	Thr	Phe	Thr	Ser	Ala	Pro	115	120	125	
Leu	Leu	Pro	Gln	Gly	Gln	Gly	Ala	Ile	Tyr	Ser	Leu	Gly	Ser	Val	Met	130	135	140	
Ile	Glu	Asn	Ser	Glu	Glu	Val	Thr	Phe	Cys	Gly	Asn	Tyr	Ser	Ser	Trp	145	150	155	160
Ser	Gly	Ala	Ala	Ile	Tyr	Thr	Pro	Tyr	Leu	Leu	Gly	Ser	Lys	Ala	Ser				

165										170					175				
Arg	Pro	Ser	Val	Asn	Leu	Ser	Gly	Asn	Arg	Tyr	Leu	Val	Phe	Arg	Asp				
			180					185					190						
Tyr	Val	Ser	Gln	Gly	Tyr	Gly	Gly	Ala	Val	Ser	Thr	His	Asn	Leu	Thr				
		195					200					205							
Leu	Thr	Thr	Arg	Gly	Pro	Ser	Cys	Phe	Glu	Asn	Asn	His	Ala	Tyr	His				
	210					215					220								
Asp	Val	Asn	Ser	Asn	Gly	Gly	Ala	Ile	Ala	Ile	Ala	Pro	Gly	Gly	Ser				
225					230					235					240				
Ile	Ser	Ile	Ser	Val	Lys	Ser	Gly	Asp	Leu	Ile	Phe	Lys	Gly	Asn	Thr				
				245					250					255					
Ala	Ser	Gln	Asp	Gly	Asn	Thr	Ile	His	Asn	Ser	Ile	His	Leu	Gln	Ser				
			260					265					270						
Gly	Ala	Gln	Phe	Lys	Asn	Leu	Arg	Ala	Val	Ser	Glu	Ser	Gly	Val	Tyr				
		275					280					285							
Phe	Tyr	Asp	Pro	Ile	Ser	His	Ser	Glu	Ser	His	Lys	Ile	Thr	Asp	Leu				
	290					295					300								
Val	Ile	Asn	Ala	Pro	Glu	Gly	Lys	Glu	Thr	Tyr	Glu	Gly	Thr	Ile	Ser				
305					310					315					320				
Phe	Ser	Gly	Leu	Cys	Leu	Asp	Asp	His	Glu	Val	Cys	Ala	Glu	Asn	Leu				
				325					330					335					
Thr	Ser	Thr	Ile	Leu	Gln	Asp	Val	Thr	Leu	Ala	Gly	Gly	Thr	Leu	Ser				
			340					345					350						
Leu	Ser	Asp	Gly	Val	Thr	Leu	Gln	Leu	His	Ser	Phe	Lys	Gln	Glu	Ala				
		355					360					365							
Ser	Ser	Thr	Leu	Thr	Met	Ser	Pro	Gly	Thr	Thr	Leu	Leu	Cys	Ser	Gly				
	370					375					380								
Asp	Ala	Arg	Val	Gln	Asn	Leu	His	Ile	Leu	Ile	Glu	Asp	Thr	Asp	Asn				
385					390					395					400				
Phe	Val	Pro	Val	Arg	Ile	Arg	Ala	Glu	Asp	Lys	Asp	Ala	Leu	Val	Ser				
				405					410					415					
Leu	Glu	Lys	Leu	Lys	Val	Ala	Phe	Glu	Ala	Tyr	Trp	Ser	Val	Tyr	Asp				
			420					425					430						
Phe	Pro	Gln	Phe	Lys	Glu	Ala	Phe	Thr	Ile	Pro	Leu	Leu	Glu	Leu	Leu				
		435					440					445							
Gly	Pro	Ser	Phe	Asp	Ser	Leu	Leu	Leu	Gly	Glu	Thr	Thr	Leu	Glu	Arg				
						455					460								
Thr	Gln	Val	Thr	Thr	Glu	Asn	Asp	Ala	Val	Arg	Gly	Phe	Trp	Ser	Leu				
465					470					475					480				

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr
 485 490 495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser
 500 505 510

Thr Pro

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 787 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAAAACGT	CTATTCGTAA	GTTCTTAATT	TCTACCACAC	TGGCGCCATG	TTTTGCTTCA	60
ACAGCGTTTA	CTGTAGAAGT	TATCATGCCT	TCCGAGAACT	TTGATGGATC	GAGTGGGAAG	120
ATTTTTCCTT	ACACAACACT	TTCTGATCCT	AGAGGGACAC	TCTGTATTTT	TTCAGGGGAT	180
CTCTACATTG	CGAATCTTGA	TAATGCCATA	TCCAGAACCT	CTTCCAGTTG	CTTTAGCAAT	240
AGGGCGGGAG	CACTACAAAT	CTTAGGAAAA	GGTGGGGTTT	TCTCCTTCTT	AAATATCCGT	300
TCTTCAGCTG	ACGGAGCCGC	GATTAGTAGT	GTAATCACCC	AAAATCCTGA	ACTATGTCCC	360
TTGAGTTTTT	CAGGATTTAG	TCAGATGATC	TTCGATAACT	GTGAATCTTT	GACTTCAGAT	420
ACCTCAGCGA	GTAATGTCAT	ACCTCACGCA	TCGGCGATTT	ACGCTACAAC	GCCCATGCTC	480
TTTACAAACA	ATGACTCCAT	ACTATTCCAA	TACAACCGTT	CTGCAGGATT	TGGAGCTGCC	540
ATTCGAGGCA	CAAGCATCAC	AATAGAAAAT	ACGAAAAAGA	GCCTTCTCTT	TAATGGTAAT	600
GGATCCATCT	CTAATGGAGG	GGCCCTCACG	GGATCTGCAG	CGATCAACCT	CATCAACAAT	660
AGCGCTCCTG	TGATTTTCTC	AACGAATGCT	ACAGGGATCT	ATGGTGGGGC	TATTTACCTT	720
ACCGGAGGAT	CTATGCTCAC	CTCTGGGAAC	CTCTCAGGAG	TCTTGTTTCG	TTATAATAGC	780
TCGCGCT						787

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Lys	Thr	Ser	Ile	Arg	Lys	Phe	Leu	Ile	Ser	Thr	Thr	Leu	Ala	Pro
1				5					10					15	
Cys	Phe	Ala	Ser	Thr	Ala	Phe	Thr	Val	Glu	Val	Ile	Met	Pro	Ser	Glu
			20					25					30		
Asn	Phe	Asp	Gly	Ser	Ser	Gly	Lys	Ile	Phe	Pro	Tyr	Thr	Thr	Leu	Ser
		35					40					45			

Asp Pro Arg Gly Thr Leu Cys Ile Phe Ser Gly Asp Leu Tyr Ile Ala
 50 55 60
 Asn Leu Asp Asn Ala Ile Ser Arg Thr Ser Ser Ser Cys Phe Ser Asn
 65 70 75 80
 Arg Ala Gly Ala Leu Gln Ile Leu Gly Lys Gly Gly Val Phe Ser Phe
 85 90 95
 Leu Asn Ile Arg Ser Ser Ala Asp Gly Ala Ala Ile Ser Ser Val Ile
 100 105 110
 Thr Gln Asn Pro Glu Leu Cys Pro Leu Ser Phe Ser Gly Phe Ser Gln
 115 120 125
 Met Ile Phe Asp Asn Cys Glu Ser Leu Thr Ser Asp Thr Ser Ala Ser
 130 135 140
 Asn Val Ile Pro His Ala Ser Ala Ile Tyr Ala Thr Thr Pro Met Leu
 145 150 155 160
 Phe Thr Asn Asn Asp Ser Ile Leu Phe Gln Tyr Asn Arg Ser Ala Gly
 165 170 175
 Phe Gly Ala Ala Ile Arg Gly Thr Ser Ile Thr Ile Glu Asn Thr Lys
 180 185 190
 Lys Ser Leu Leu Phe Asn Gly Asn Gly Ser Ile Ser Asn Gly Gly Ala
 195 200 205
 Leu Thr Gly Ser Ala Ala Ile Asn Leu Ile Asn Asn Ser Ala Pro Val
 210 215 220
 Ile Phe Ser Thr Asn Ala Thr Gly Ile Tyr Gly Gly Ala Ile Tyr Leu
 225 230 235 240
 Thr Gly Gly Ser Met Leu Thr Ser Gly Asn Leu Ser Gly Val Leu Phe
 245 250 255
 Val Tyr Asn Ser Ser Arg
 260

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2838 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGAAGACTT	CAGTTTCTAT	GTTGTTGGCC	CTGCTTTGCT	CGGGGGCTAG	CTCTATTGTA	60
CTCCATGCCG	CAACCACTCC	ACTAAATCCT	GAAGATGGGT	TTATTGGGGA	GGGCAATACA	120
AATACTTTTT	CTCCGAAATC	TACAACGGAT	GCTGCAGGAA	CTACCTACTC	TCTCACAGGA	180
GAGGTTCTGT	TTATAGATCC	GGGGAAAGGT	GTTTCAATTA	CAGGAAGTTG	CTTTGTAGAA	240

ACTGCTGGCG	ATCTTACATT	TTTAGGTAAT	GGAAATACCC	TAAAGTTCCT	GTCGGTAGAT	300
GCAGGTGCTA	ATATCGCGGT	TGCTCATGTA	CAAGGAAGTA	AGAATTTAAG	CTTCACAGAT	360
TTCCTTTCTC	TGGTGATCAC	AGAATCTCCA	AAATCCGCTG	TTAGTACAGG	AAAAGGTAGC	420
CTAGTCAGTT	CAGGTGCAGT	CCAACTGCAA	GATATAAACA	CTCTAGTTCT	TACAAGCAAT	480
GCCTCTGTCT	AAGATGGTGG	CGTGATTAAA	GGAAACTCCT	GCTTGATTCA	GGGAATCAAA	540
AATAGTGCGA	TTTTTGGACA	AAATACATCT	TCGAAAAAAG	GAGGGGCGAT	CTCCACGACT	600
CAAGGACTCA	CCATAGAGAA	TAACTTAGGG	ACGCTAAAGT	TCAATGAAAA	CAAAGCAGTG	660
ACCTCAGGAG	GCGCCTTAGA	TTTAGGAGCC	GCGTCTACAT	TCACTGCGAA	CCATGAGTTG	720
ATATTTTTCAC	AAAATAAGAC	TTCTGGGAAT	GCTGCAAATG	GCGGAGCCAT	AAATTGCTCA	780
GGCGACCTAA	CATTTACTGA	TAACACTTCT	TTGTTACTTC	AAGAAAATAG	CACAATGCAG	840
GATGGTGGAG	CTTTGTGTAG	CACAGGAACC	ATAAGCATTA	CCGGTAGTGA	TTCTATCAAT	900
GTGATAGGAA	ATACTTCAGG	ACAAAAAGGA	GGAGCGATTT	CTGCAGCTTC	TCTCAAGATT	960
TTGGGAGGGC	AGGGAGGCGC	TCTCTTTTCT	AATAACGTAG	TGACTCATGC	CACCCCTCTA	1020
GGAGGTGCCA	TTTTTATCAA	CACAGGAGGA	TCCTTGCGAGC	TCTTCACTCA	AGGAGGGGGAT	1080
ATCGTATTCG	AGGGGAATCA	GGTCACTACA	ACAGCTCCAA	ATGCTACCAC	TAAGAGAAAT	1140
GTAATTCACC	TCGAGAGCAC	CGCGAAGTGG	ACGGGACTTG	CTGCAAGTCA	AGGTAACGCT	1200
ATCTATTTCT	ATGATCCCAT	TACCACCAAC	GATACGGGAG	CAAGCGATAA	CTTACGTATC	1260
AATGAGGTCA	GTGCAAATCA	AAAGCTCTCG	GGATCTATAG	TATTTTCTGG	AGAGAGATTG	1320
TCGACAGCAG	AAGCTATAGC	TGAAAACTCT	ACTTCGAGGA	TCAACCAGCC	TGTCACTTTA	1380
GTAGAGGGGA	GCTTAGAACT	TAAACAGGGA	GTGACCTTGA	TCACACAAGG	ATTCTCGCAG	1440
GAGCCAGAAT	CCACGCTTCT	TTTGGATTTG	GGGACCTCAT	TACAAGCTTC	TACAGAAGAT	1500
ATCGTCATCA	CAAATTCATC	TATAAATGCC	GATACCATTT	ACGGAAAGAA	TCCAATCAAT	1560
ATTGTAGCTT	CAGCAGCGAA	TAAGAACATT	ACCCTAACAG	GAACCTTAGC	ACTTGTAAT	1620
GCAGATGGAG	CTTTGTATGA	GAACCATACC	TTGCAAGACT	CTCAAGATTA	TAGCTTTGTA	1680
AAGTTATCTC	CAGGAGCGGG	AGGGACTATA	ATTACTCAAG	ATGCTTCTCA	GAAGCTTCTT	1740
GAAGTAGCTC	CTTCTAGACC	ACATTATGGC	TATCAAGGAC	ATTGGAATGT	GCAAGTCATC	1800
CCAGGAACGG	GAACTCAACC	GAGCCAGGCA	AATTTAGAAT	GGGTGCGGAC	AGGATACCTT	1860
CCGAATCCCG	AACGGCAAGG	ATTTTGTAGT	CCCAATAGCC	TGTGGGGTTC	TTTTGTGAT	1920
CAGCGTGCTA	TCCAAGAAAT	CATGGTAAAT	AGTAGCCAAA	TCTTATGTCA	GGAACGGGGA	1980
GTCTGGGGAG	CTGGAATTGC	TAATTTCCCTA	CATAGAGATA	AAATTAATGA	GCACGGCTAT	2040
CGCCATAGCG	GTGTCGGTTA	TCTTGTGGGA	GTTGGCACTC	ATGCTTTTTT	TGATGCTACG	2100
ATAAATGCGG	CTTTTTGCCA	GCTCTTCAGT	AGAGATAAAG	ACTACGTAGT	ATCCAAAAAT	2160
CATGGAACCT	GCTACTCAGG	GGTCGTATTT	CTTGAGGATA	CCCTAGAGTT	TAGAAGTCCA	2220
CAGGGATTCT	ATACTGATAG	CTCCTCAGAA	GCTTGCTGTA	ACCAAGTCGT	CACTATAGAT	2280
ATGCAGTTGT	CTTACAGCCA	TAGAAAATAAT	GATATGAAAA	CCAAATACAC	GACATATCCA	2340
GAAGCTCAGG	GATCTTGGGC	AAATGATGTT	TTTGGTCTTG	AGTTTGGAGC	GACTACATAC	2400
TACTACCCTA	ACAGTACTTT	TTTATTTGAT	TACTACTCTC	CGTTTCTCAG	GCTGCAGTGC	2460
ACCTATGCTC	ACCAGGAAGA	CTTCAAAGAG	ACAGGAGGTG	AGGTTCGTCA	CTTTACTAGC	2520
GGAGATCTTT	TCAATTTAGC	AGTTCCTATT	GGCGTGAAGT	TTGAGAGATT	TTCAGACTGT	2580
AAAAGGGGAT	CTTATGAACT	TACCCTTGCT	TATGTTCCCTG	ATGTGATTCTG	CAAAGATCCC	2640
AAGAGCACGG	CAACATTGGC	TAGTGGAGCT	ACGTGGAGCA	CCCACGGAAA	CAATCTCTCC	2700
AGACAAGGAT	TACAACTGCG	TTTAGGGGAA	CACTGTCTCA	TAAATCCTGG	AATTGAGGTG	2760
TTCAGTCACG	GAGCTATTGA	ATTGCGGGGA	TCCTCTCGTA	ATTATAACAT	CAATCTCGGG	2820
GGTAAATACC	GATTTTAA					2838

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Lys Thr Ser Val Ser Met Leu Leu Ala Leu Leu Cys Ser Gly Ala

1	5	10	15
Ser Ser Ile Val	Leu His Ala Ala	Thr Thr Pro Leu Asn	Pro Glu Asp
20		25	30
Gly Phe Ile Gly	Glu Gly Asn Thr	Asn Thr Phe Ser	Pro Lys Ser Thr
35	40	45	
Thr Asp Ala Ala	Gly Thr Thr Tyr	Ser Leu Thr Gly	Glu Val Leu Phe
50	55	60	
Ile Asp Pro Gly	Lys Gly Gly Ser	Ile Thr Gly Thr	Cys Phe Val Glu
65	70	75	80
Thr Ala Gly Asp	Leu Thr Phe Leu	Gly Asn Gly Asn	Thr Leu Lys Phe
	85	90	95
Leu Ser Val Asp	Ala Gly Ala Asn	Ile Ala Val Ala	His Val Gln Gly
100		105	110
Ser Lys Asn Leu	Ser Phe Thr Asp	Phe Leu Ser Leu	Val Ile Thr Glu
115	120	125	
Ser Pro Lys Ser	Ala Val Ser Thr	Gly Lys Gly Ser	Leu Val Ser Ser
130	135	140	
Gly Ala Val Gln	Leu Gln Asp Ile	Asn Thr Leu Val	Leu Thr Ser Asn
145	150	155	160
Ala Ser Val Glu	Asp Gly Gly Val	Ile Lys Gly Asn	Ser Cys Leu Ile
165	170	175	
Gln Gly Ile Lys	Asn Ser Ala Ile	Phe Gly Gln Asn	Thr Ser Ser Lys
180	185	190	
Lys Gly Gly Ala	Ile Ser Thr Thr	Gln Gly Leu Thr	Ile Glu Asn Asn
195	200	205	
Leu Gly Thr Leu	Lys Phe Asn Glu	Asn Lys Ala Val	Thr Ser Gly Gly
210	215	220	
Ala Leu Asp Leu	Gly Ala Ala Ser	Thr Phe Thr Ala	Asn His Glu Leu
225	230	235	240
Ile Phe Ser Gln	Asn Lys Thr Ser	Gly Asn Ala Ala	Asn Gly Gly Ala
245	250	255	
Ile Asn Cys Ser	Gly Asp Leu Thr	Phe Thr Asp Asn	Thr Ser Leu Leu
260	265	270	
Leu Gln Glu Asn	Ser Thr Met Gln	Asp Gly Gly Ala	Leu Cys Ser Thr
275	280	285	
Gly Thr Ile Ser	Ile Thr Gly Ser	Asp Ser Ile Asn	Val Ile Gly Asn
290	295	300	
Thr Ser Gly Gln	Lys Gly Gly Ala	Ile Ser Ala Ala	Ser Leu Lys Ile
305	310	315	320

Leu Gly Gly Gln Gly Gly Ala Leu Phe Ser Asn Asn Val Val Thr His
 325 330 335
 Ala Thr Pro Leu Gly Gly Ala Ile Phe Ile Asn Thr Gly Gly Ser Leu
 340 345 350
 Gln Leu Phe Thr Gln Gly Gly Asp Ile Val Phe Glu Gly Asn Gln Val
 355 360 365
 Thr Thr Thr Ala Pro Asn Ala Thr Thr Lys Arg Asn Val Ile His Leu
 370 375 380
 Glu Ser Thr Ala Lys Trp Thr Gly Leu Ala Ala Ser Gln Gly Asn Ala
 385 390 395 400
 Ile Tyr Phe Tyr Asp Pro Ile Thr Thr Asn Asp Thr Gly Ala Ser Asp
 405 410 415
 Asn Leu Arg Ile Asn Glu Val Ser Ala Asn Gln Lys Leu Ser Gly Ser
 420 425 430
 Ile Val Phe Ser Gly Glu Arg Leu Ser Thr Ala Glu Ala Ile Ala Glu
 435 440 445
 Asn Leu Thr Ser Arg Ile Asn Gln Pro Val Thr Leu Val Glu Gly Ser
 450 455 460
 Leu Glu Leu Lys Gln Gly Val Thr Leu Ile Thr Gln Gly Phe Ser Gln
 465 470 475 480
 Glu Pro Glu Ser Thr Leu Leu Leu Asp Leu Gly Thr Ser Leu Gln Ala
 485 490 495
 Ser Thr Glu Asp Ile Val Ile Thr Asn Ser Ser Ile Asn Ala Asp Thr
 500 505 510
 Ile Tyr Gly Lys Asn Pro Ile Asn Ile Val Ala Ser Ala Ala Asn Lys
 515 520 525
 Asn Ile Thr Leu Thr Gly Thr Leu Ala Leu Val Asn Ala Asp Gly Ala
 530 535 540
 Leu Tyr Glu Asn His Thr Leu Gln Asp Ser Gln Asp Tyr Ser Phe Val
 545 550 555 560
 Lys Leu Ser Pro Gly Ala Gly Gly Thr Ile Ile Thr Gln Asp Ala Ser
 565 570 575
 Gln Lys Leu Leu Glu Val Ala Pro Ser Arg Pro His Tyr Gly Tyr Gln
 580 585 590
 Gly His Trp Asn Val Gln Val Ile Pro Gly Thr Gly Thr Gln Pro Ser
 595 600 605
 Gln Ala Asn Leu Glu Trp Val Arg Thr Gly Tyr Leu Pro Asn Pro Glu
 610 615 620

Arg	Gln	Gly	Phe	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Phe	Val	Asp	625	630	635	640
Gln	Arg	Ala	Ile	Gln	Glu	Ile	Met	Val	Asn	Ser	Ser	Gln	Ile	Leu	Cys	645	650		655
Gln	Glu	Arg	Gly	Val	Trp	Gly	Ala	Gly	Ile	Ala	Asn	Phe	Leu	His	Arg	660	665		670
Asp	Lys	Ile	Asn	Glu	His	Gly	Tyr	Arg	His	Ser	Gly	Val	Gly	Tyr	Leu	675	680		685
Val	Gly	Val	Gly	Thr	His	Ala	Phe	Ser	Asp	Ala	Thr	Ile	Asn	Ala	Ala	690	695	700	
Phe	Cys	Gln	Leu	Phe	Ser	Arg	Asp	Lys	Asp	Tyr	Val	Val	Ser	Lys	Asn	705	710	715	720
His	Gly	Thr	Ser	Tyr	Ser	Gly	Val	Val	Phe	Leu	Glu	Asp	Thr	Leu	Glu	725	730		735
Phe	Arg	Ser	Pro	Gln	Gly	Phe	Tyr	Thr	Asp	Ser	Ser	Ser	Glu	Ala	Cys	740	745		750
Cys	Asn	Gln	Val	Val	Thr	Ile	Asp	Met	Gln	Leu	Ser	Tyr	Ser	His	Arg	755	760		765
Asn	Asn	Asp	Met	Lys	Thr	Lys	Tyr	Thr	Thr	Tyr	Pro	Glu	Ala	Gln	Gly	770	775	780	
Ser	Trp	Ala	Asn	Asp	Val	Phe	Gly	Leu	Glu	Phe	Gly	Ala	Thr	Thr	Tyr	785	790	795	800
Tyr	Tyr	Pro	Asn	Ser	Thr	Phe	Leu	Phe	Asp	Tyr	Tyr	Ser	Pro	Phe	Leu	805	810		815
Arg	Leu	Gln	Cys	Thr	Tyr	Ala	His	Gln	Glu	Asp	Phe	Lys	Glu	Thr	Gly	820	825		830
Gly	Glu	Val	Arg	His	Phe	Thr	Ser	Gly	Asp	Leu	Phe	Asn	Leu	Ala	Val	835	840		845
Pro	Ile	Gly	Val	Lys	Phe	Glu	Arg	Phe	Ser	Asp	Cys	Lys	Arg	Gly	Ser	850	855	860	
Tyr	Glu	Leu	Thr	Leu	Ala	Tyr	Val	Pro	Asp	Val	Ile	Arg	Lys	Asp	Pro	865	870	875	880
Lys	Ser	Thr	Ala	Thr	Leu	Ala	Ser	Gly	Ala	Thr	Trp	Ser	Thr	His	Gly	885	890		895
Asn	Asn	Leu	Ser	Arg	Gln	Gly	Leu	Gln	Leu	Arg	Leu	Gly	Asn	His	Cys	900	905		910
Leu	Ile	Asn	Pro	Gly	Ile	Glu	Val	Phe	Ser	His	Gly	Ala	Ile	Glu	Leu	915	920		925
Arg	Gly	Ser	Ser	Arg	Asn	Tyr	Asn	Ile	Asn	Leu	Gly	Gly	Lys	Tyr	Arg				

930

935

940

Phe
945

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 259...3000
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATCAGGTGAT AAAAGTTCCT CGTTAGCTAG TGA	CTGTAGG TGACATGAGA AAGCTAACAC	60
GGAGGAAACT AAAACCCAAG GAATCGAAGT C	TTTCATGGTA ATGCTTTTGT TTTT	120
ACTATTCGCA TCAATATAGA AACAAAATAA G	TAAATCAAG TTAAAGATGA CAAAACAGCT	180
GTCAAGAATT TTTATCTTGA CTCTCTGAGT T	TTTCTATTTT ATATGACGCA AGTAAGAATT	240
TAATAATAAA GTGGGTTT ATG AAA TCG CAA	TTT TCC TGG TTA GTG CTC TCT	291
Met Lys Ser Gln Phe Ser Trp Leu Val Leu Ser		
1 5 10		
TCG ACA TTG GCA TGT TTT ACT AGT TGT	TCC ACT GTT TTT GCT GCA ACT	339
Ser Thr Leu Ala Cys Phe Thr Ser Cys	Ser Thr Val Phe Ala Ala Thr	
15 20 25		
GCT GAA AAT ATA GGC CCC TCT GAT AGC	TTT GAC GGA AGT ACT AAC ACA	387
Ala Glu Asn Ile Gly Pro Ser Asp Ser	Phe Asp Gly Ser Thr Asn Thr	
30 35 40		
GGC ACC TAT ACT CCT AAA AAT ACG ACT	ACT ACT GGA ATA GAC TAT ACT CTG	435
Gly Thr Tyr Thr Pro Lys Asn Thr Thr	Gly Ile Asp Tyr Thr Leu	
45 50 55		
ACA GGA GAT ATA ACT CTG CAA AAC CTT	GGG GAT TCG GCA GCT TTA ACG	483
Thr Gly Asp Ile Thr Leu Gln Asn Leu	Gly Asp Ser Ala Ala Leu Thr	
60 65 70 75		
AAG GGT TGT TTT TCT GAC ACT ACG GAA	TCT TTA AGC TTT GCC GGT AAG	531
Lys Gly Cys Phe Ser Asp Thr Thr Glu	Ser Leu Ser Phe Ala Gly Lys	
80 85 90		
GGG TAC TCA CTT TCT TTT TTA AAT ATT	AAG TCT AGT GCT GAA GGC GCA	579
Gly Tyr Ser Leu Ser Phe Leu Asn Ile	Lys Ser Ser Ala Glu Gly Ala	
95 100 105		
GCA CTT TCT GTT ACA ACT GAT AAA AAT	CTG TCG CTA ACA GGA TTT TCG	627

Ala	Leu	Ser	Val	Thr	Thr	Asp	Lys	Asn	Leu	Ser	Leu	Thr	Gly	Phe	Ser	
	110						115					120				
AGT	CTT	ACT	TTC	TTA	GCG	GCC	CCA	TCA	TCG	GTA	ATC	ACA	ACC	CCC	TCA	675
Ser	Leu	Thr	Phe	Leu	Ala	Ala	Pro	Ser	Ser	Val	Ile	Thr	Thr	Pro	Ser	
	125					130				135						
GGA	AAA	GGT	GCA	GTT	AAA	TGT	GGA	GGG	GAT	CTT	ACA	TTT	GAT	AAC	AAT	723
Gly	Lys	Gly	Ala	Val	Lys	Cys	Gly	Gly	Asp	Leu	Thr	Phe	Asp	Asn	Asn	
140					145					150					155	
GGA	ACT	ATT	TTA	TTT	AAA	CAA	GAT	TAC	TGT	GAG	GAA	AAT	GGC	GGA	GCC	771
Gly	Thr	Ile	Leu	Phe	Lys	Gln	Asp	Tyr	Cys	Glu	Glu	Asn	Gly	Gly	Ala	
				160				165							170	
ATT	TCT	ACC	AAG	AAT	CTT	TCT	TTG	AAA	AAC	AGC	ACG	GGA	TCG	ATT	TCT	819
Ile	Ser	Thr	Lys	Asn	Leu	Ser	Leu	Lys	Asn	Ser	Thr	Gly	Ser	Ile	Ser	
			175					180					185			
TTT	GAA	GGG	AAT	AAA	TCG	AGC	GCA	ACA	GGG	AAA	AAA	GGT	GGG	GCT	ATT	867
Phe	Glu	Gly	Asn	Lys	Ser	Ser	Ala	Thr	Gly	Lys	Lys	Gly	Gly	Ala	Ile	
	190						195					200				
TGT	GCT	ACT	GGT	ACT	GTA	GAT	ATT	ACA	AAT	AAT	ACG	GCT	CCT	ACC	CTC	915
Cys	Ala	Thr	Gly	Thr	Val	Asp	Ile	Thr	Asn	Asn	Thr	Ala	Pro	Thr	Leu	
	205					210					215					
TTC	TCG	AAC	AAT	ATT	GCT	GAA	GCT	GCA	GGT	GGA	GCT	ATA	AAT	AGC	ACA	963
Phe	Ser	Asn	Asn	Ile	Ala	Glu	Ala	Ala	Gly	Gly	Ala	Ile	Asn	Ser	Thr	
220					225					230					235	
GGA	AAC	TGT	ACA	ATT	ACA	GGG	AAT	ACG	TCT	CTT	GTA	TTT	TCT	GAA	AAT	1011
Gly	Asn	Cys	Thr	Ile	Thr	Gly	Asn	Thr	Ser	Leu	Val	Phe	Ser	Glu	Asn	
				240					245					250		
AGT	GTG	ACA	GCG	ACC	GCA	GGA	AAT	GGA	GGA	GCT	CTT	TCT	GGA	GAT	GCC	1059
Ser	Val	Thr	Ala	Thr	Ala	Gly	Asn	Gly	Gly	Ala	Leu	Ser	Gly	Asp	Ala	
			255					260					265			
GAT	GTT	ACC	ATA	TCT	GGG	AAT	CAG	AGT	GTA	ACT	TTC	TCA	GGA	AAC	CAA	1107
Asp	Val	Thr	Ile	Ser	Gly	Asn	Gln	Ser	Val	Thr	Phe	Ser	Gly	Asn	Gln	
		270					275					280				
GCT	GTA	GCT	AAT	GGC	GGA	GCC	ATT	TAT	GCT	AAG	AAG	CTT	ACA	CTG	GCT	1155
Ala	Val	Ala	Asn	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu	Thr	Leu	Ala	
	285					290					295					
TCC	GGG	GGG	GGG	GGG	GGT	ATC	TCC	TTT	TCT	AAC	AAT	ATA	GTC	CAA	GGT	1203
Ser	Gly	Gly	Gly	Gly	Gly	Ile	Ser	Phe	Ser	Asn	Asn	Ile	Val	Gln	Gly	
300					305					310					315	
ACC	ACT	GCA	GGT	AAT	GGT	GGA	GCC	ATT	TCT	ATA	CTG	GCA	GCT	GGA	GAG	1251
Thr	Thr	Ala	Gly	Asn	Gly	Gly	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Gly	Glu	
				320					325					330		
TGT	AGT	CTT	TCA	GCA	GAA	GCA	GGG	GAC	ATT	ACC	TTC	AAT	GGG	AAT	GCC	1299
Cys	Ser	Leu	Ser	Ala	Glu	Ala	Gly	Asp	Ile	Thr	Phe	Asn	Gly	Asn	Ala	
			335					340					345			

ATT	GTT	GCA	ACT	ACA	CCA	CAA	ACT	ACA	AAA	AGA	AAT	TCT	ATT	GAC	ATA	1347
Ile	Val	Ala	Thr	Thr	Pro	Gln	Thr	Thr	Lys	Arg	Asn	Ser	Ile	Asp	Ile	
		350					355					360				
GGA	TCT	ACT	GCA	AAG	ATC	ACG	AAT	TTA	CGT	GCA	ATA	TCT	GGG	CAT	AGC	1395
Gly	Ser	Thr	Ala	Lys	Ile	Thr	Asn	Leu	Arg	Ala	Ile	Ser	Gly	His	Ser	
	365					370					375					
ATC	TTT	TTC	TAC	GAT	CCG	ATT	ACT	GCT	AAT	ACG	GCT	GCG	GAT	TCT	ACA	1443
Ile	Phe	Phe	Tyr	Asp	Pro	Ile	Thr	Ala	Asn	Thr	Ala	Ala	Asp	Ser	Thr	
380					385					390					395	
GAT	ACT	TTA	AAT	CTC	AAT	AAG	GCT	GAT	GCA	GGT	AAT	AGT	ACA	GAT	TAT	1491
Asp	Thr	Leu	Asn	Leu	Asn	Lys	Ala	Asp	Ala	Gly	Asn	Ser	Thr	Asp	Tyr	
				400					405					410		
AGT	GGG	TCG	ATT	GTT	TTT	TCT	GGT	GAA	AAG	CTC	TCT	GAA	GAT	GAA	GCA	1539
Ser	Gly	Ser	Ile	Val	Phe	Ser	Gly	Glu	Lys	Leu	Ser	Glu	Asp	Glu	Ala	
			415					420					425			
AAA	GTT	GCA	GAC	AAC	CTC	ACT	TCT	ACG	CTG	AAG	CAG	CCT	GTA	ACT	CTA	1587
Lys	Val	Ala	Asp	Asn	Leu	Thr	Ser	Thr	Leu	Lys	Gln	Pro	Val	Thr	Leu	
		430					435					440				
ACT	GCA	GGA	AAT	TTA	GTA	CTT	AAA	CGT	GGT	GTC	ACT	CTC	GAT	ACG	AAA	1635
Thr	Ala	Gly	Asn	Leu	Val	Leu	Lys	Arg	Gly	Val	Thr	Leu	Asp	Thr	Lys	
	445					450					455					
GGC	TTT	ACT	CAG	ACC	GCG	GGT	TCC	TCT	GTT	ATT	ATG	GAT	GCG	GGC	ACA	1683
Gly	Phe	Thr	Gln	Thr	Ala	Gly	Ser	Ser	Val	Ile	Met	Asp	Ala	Gly	Thr	
460					465					470					475	
ACG	TTA	AAA	GCA	AGT	ACA	GAG	GAG	GTC	ACT	TTA	ACA	GGT	CTT	TCC	ATT	1731
Thr	Leu	Lys	Ala	Ser	Thr	Glu	Glu	Val	Thr	Leu	Thr	Gly	Leu	Ser	Ile	
				480					485						490	
CCT	GTA	GAC	TCT	TTA	GGC	GAG	GGT	AAG	AAA	GTT	GTA	ATT	GCT	GCT	TCT	1779
Pro	Val	Asp	Ser	Leu	Gly	Glu	Gly	Lys	Lys	Val	Val	Ile	Ala	Ala	Ser	
			495					500					505			
GCA	GCA	AGT	AAA	AAT	GTA	GCC	CTT	AGT	GGT	CCG	ATT	CTT	CTT	TTG	GAT	1827
Ala	Ala	Ser	Lys	Asn	Val	Ala	Leu	Ser	Gly	Pro	Ile	Leu	Leu	Leu	Asp	
		510					515					520				
AAC	CAA	GGG	AAT	GCT	TAT	GAA	AAT	CAC	GAC	TTA	GGA	AAA	ACT	CAA	GAC	1875
Asn	Gln	Gly	Asn	Ala	Tyr	Glu	Asn	His	Asp	Leu	Gly	Lys	Thr	Gln	Asp	
	525					530					535					
TTT	TCA	TTT	GTG	CAG	CTC	TCT	GCT	CTG	GGT	ACT	GCA	ACA	ACT	ACA	GAT	1923
Phe	Ser	Phe	Val	Gln	Leu	Ser	Ala	Leu	Gly	Thr	Ala	Thr	Thr	Thr	Asp	
540					545					550					555	
GTT	CCA	GCG	GTT	CCT	ACA	GTA	GCA	ACT	CCT	ACG	CAC	TAT	GGG	TAT	CAA	1971
Val	Pro	Ala	Val	Pro	Thr	Val	Ala	Thr	Pro	Thr	His	Tyr	Gly	Tyr	Gln	
				560					565					570		
GGT	ACT	TGG	GGA	ATG	ACT	TGG	GTT	GAT	GAT	ACC	GCA	AGC	ACT	CCA	AAG	2019

Gly	Thr	Trp	Gly	Met	Thr	Trp	Val	Asp	Asp	Thr	Ala	Ser	Thr	Pro	Lys	
			575					580					585			
ACT	AAG	ACA	GCG	ACA	TTA	GCT	TGG	ACC	AAT	ACA	GGC	TAC	CTT	CCG	AAT	2067
Thr	Lys	Thr	Ala	Thr	Leu	Ala	Trp	Thr	Asn	Thr	Gly	Tyr	Leu	Pro	Asn	
			590				595					600				
CCT	GAG	CGT	CAA	GGA	CCT	TTA	GTT	CCT	AAT	AGC	CTT	TGG	GGA	TCT	TTT	2115
Pro	Glu	Arg	Gln	Gly	Pro	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Phe	
	605					610					615					
TCA	GAC	ATC	CAA	GCG	ATT	CAA	GGT	GTC	ATA	GAG	AGA	AGT	GCT	TTG	ACT	2163
Ser	Asp	Ile	Gln	Ala	Ile	Gln	Gly	Val	Ile	Glu	Arg	Ser	Ala	Leu	Thr	
620					625					630					635	
CTT	TGT	TCA	GAT	CGA	GGC	TTC	TGG	GCT	GCG	GGA	GTC	GCC	AAT	TTC	TTA	2211
Leu	Cys	Ser	Asp	Arg	Gly	Phe	Trp	Ala	Ala	Gly	Val	Ala	Asn	Phe	Leu	
				640					645					650		
GAT	AAA	GAT	AAG	AAA	GGG	GAA	AAA	CGC	AAA	TAC	CGT	CAT	AAA	TCT	GGT	2259
Asp	Lys	Asp	Lys	Lys	Gly	Glu	Lys	Arg	Lys	Tyr	Arg	His	Lys	Ser	Gly	
			655					660					665			
GGA	TAT	GCT	ATC	GGA	GGT	GCA	GCG	CAA	ACT	TGT	TCT	GAA	AAC	TTA	ATT	2307
Gly	Tyr	Ala	Ile	Gly	Gly	Ala	Ala	Gln	Thr	Cys	Ser	Glu	Asn	Leu	Ile	
		670					675					680				
AGC	TTT	GCC	TTT	TGC	CAA	CTC	TTT	GGT	AGC	GAT	AAA	GAT	TTC	TTA	GTC	2355
Ser	Phe	Ala	Phe	Cys	Gln	Leu	Phe	Gly	Ser	Asp	Lys	Asp	Phe	Leu	Val	
	685					690					695					
GCT	AAA	AAT	CAT	ACT	GAT	ACC	TAT	GCA	GGA	GCC	TTC	TAT	ATC	CAA	CAC	2403
Ala	Lys	Asn	His	Thr	Asp	Thr	Tyr	Ala	Gly	Ala	Phe	Tyr	Ile	Gln	His	
700					705					710					715	
ATT	ACA	GAA	TGT	AGT	GGG	TTC	ATA	GGT	TGT	CTC	TTA	GAT	AAA	CTT	CCT	2451
Ile	Thr	Glu	Cys	Ser	Gly	Phe	Ile	Gly	Cys	Leu	Leu	Asp	Lys	Leu	Pro	
				720					725					730		
GGC	TCT	TGG	AGT	CAT	AAA	CCC	CTC	GTT	TTA	GAA	GGG	CAG	CTC	GCT	TAT	2499
Gly	Ser	Trp	Ser	His	Lys	Pro	Leu	Val	Leu	Glu	Gly	Gln	Leu	Ala	Tyr	
			735					740					745			
AGC	CAC	GTC	AGT	AAT	GAT	CTG	AAG	ACA	AAG	TAT	ACT	GCG	TAT	CCT	GAG	2547
Ser	His	Val	Ser	Asn	Asp	Leu	Lys	Thr	Lys	Tyr	Thr	Ala	Tyr	Pro	Glu	
		750					755					760				
GTG	AAA	GGT	TCT	TGG	GGG	AAT	AAT	GCT	TTT	AAC	ATG	ATG	TTG	GGA	GCT	2595
Val	Lys	Gly	Ser	Trp	Gly	Asn	Asn	Ala	Phe	Asn	Met	Met	Leu	Gly	Ala	
	765					770					775					
TCT	TCT	CAT	TCT	TAT	CCT	GAA	TAC	CTG	CAT	TGT	TTT	GAT	ACC	TAT	GCT	2643
Ser	Ser	His	Ser	Tyr	Pro	Glu	Tyr	Leu	His	Cys	Phe	Asp	Thr	Tyr	Ala	
780					785					790					795	
CCA	TAC	ATC	AAA	CTG	AAT	CTG	ACC	TAT	ATA	CGT	CAG	GAC	AGC	TTC	TCG	2691
Pro	Tyr	Ile	Lys	Leu	Asn	Leu	Thr	Tyr	Ile	Arg	Gln	Asp	Ser	Phe	Ser	
				800					805					810		

GAG AAA GGT ACA GAA GGA AGA TCT TTT GAT GAC AGC AAC CTC TTC AAT	2739
Glu Lys Gly Thr Glu Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn	
815 820 825	
TTA TCT TTG CCT ATA GGG GTG AAG TTT GAG AAG TTC TCT GAT TGT AAT	2787
Leu Ser Leu Pro Ile Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn	
830 835 840	
GAC TTT TCT TAT GAT CTG ACT TTA TCC TAT GTT CCT GAT CTT ATC CGC	2835
Asp Phe Ser Tyr Asp Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg	
845 850 855	
AAT GAT CCC AAA TGC ACT ACA GCA CTT GTA ATC AGC GGA GCC TCT TGG	2883
Asn Asp Pro Lys Cys Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp	
860 865 870 875	
GAA ACT TAT GCC AAT AAC TTA GCA CGA CAG GCC TTG CAA GTG CGT GCA	2931
Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala	
880 885 890	
GGC AGT CAC TAC GCC TTC TCT CCT ATG TTT GAA GTG CTC GGC CAG TTT	2979
Gly Ser His Tyr Ala Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe	
895 900 905	
GTC TTT GAA GTT CGT GGA TCC	3000
Val Phe Glu Val Arg Gly Ser	
910	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Lys Ser Gln Phe Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys	
1 5 10 15	
Phe Thr Ser Cys Ser Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly	
20 25 30	
Pro Ser Asp Ser Phe Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro	
35 40 45	
Lys Asn Thr Thr Thr Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr	
50 55 60	
Leu Gln Asn Leu Gly Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser	
65 70 75 80	

Asp	Thr	Thr	Glu	Ser	Leu	Ser	Phe	Ala	Gly	Lys	Gly	Tyr	Ser	Leu	Ser		
				85					90					95			
Phe	Leu	Asn	Ile	Lys	Ser	Ser	Ala	Glu	Gly	Ala	Ala	Leu	Ser	Val	Thr		
			100					105					110				
Thr	Asp	Lys	Asn	Leu	Ser	Leu	Thr	Gly	Phe	Ser	Ser	Leu	Thr	Phe	Leu		
		115					120					125					
Ala	Ala	Pro	Ser	Ser	Val	Ile	Thr	Thr	Pro	Ser	Gly	Lys	Gly	Ala	Val		
	130					135					140						
Lys	Cys	Gly	Gly	Asp	Leu	Thr	Phe	Asp	Asn	Asn	Gly	Thr	Ile	Leu	Phe		
145					150				155						160		
Lys	Gln	Asp	Tyr	Cys	Glu	Glu	Asn	Gly	Gly	Ala	Ile	Ser	Thr	Lys	Asn		
			165					170						175			
Leu	Ser	Leu	Lys	Asn	Ser	Thr	Gly	Ser	Ile	Ser	Phe	Glu	Gly	Asn	Lys		
			180					185					190				
Ser	Ser	Ala	Thr	Gly	Lys	Lys	Gly	Gly	Ala	Ile	Cys	Ala	Thr	Gly	Thr		
		195					200					205					
Val	Asp	Ile	Thr	Asn	Asn	Thr	Ala	Pro	Thr	Leu	Phe	Ser	Asn	Asn	Ile		
	210					215					220						
Ala	Glu	Ala	Ala	Gly	Gly	Ala	Ile	Asn	Ser	Thr	Gly	Asn	Cys	Thr	Ile		
225				230					235						240		
Thr	Gly	Asn	Thr	Ser	Leu	Val	Phe	Ser	Glu	Asn	Ser	Val	Thr	Ala	Thr		
				245					250					255			
Ala	Gly	Asn	Gly	Gly	Ala	Leu	Ser	Gly	Asp	Ala	Asp	Val	Thr	Ile	Ser		
		260						265					270				
Gly	Asn	Gln	Ser	Val	Thr	Phe	Ser	Gly	Asn	Gln	Ala	Val	Ala	Asn	Gly		
	275					280					285						
Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu	Thr	Leu	Ala	Ser	Gly	Gly	Gly	Gly		
	290				295						300						
Gly	Ile	Ser	Phe	Ser	Asn	Asn	Ile	Val	Gln	Gly	Thr	Thr	Ala	Gly	Asn		
305					310				315						320		
Gly	Gly	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Gly	Glu	Cys	Ser	Leu	Ser	Ala		
				325					330					335			
Glu	Ala	Gly	Asp	Ile	Thr	Phe	Asn	Gly	Asn	Ala	Ile	Val	Ala	Thr	Thr		
			340					345					350				
Pro	Gln	Thr	Thr	Lys	Arg	Asn	Ser	Ile	Asp	Ile	Gly	Ser	Thr	Ala	Lys		
		355				360						365					
Ile	Thr	Asn	Leu	Arg	Ala	Ile	Ser	Gly	His	Ser	Ile	Phe	Phe	Tyr	Asp		
	370					375					380						

Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu
 385 390 395 400
 Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val
 405 410 415
 Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn
 420 425 430
 Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu
 435 440 445
 Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr
 450 455 460
 Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser
 465 470 475 480
 Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu
 485 490 495
 Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn
 500 505 510
 Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala
 515 520 525
 Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln
 530 535 540
 Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro
 545 550 555 560
 Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met
 565 570 575
 Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr
 580 585 590
 Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly
 595 600 605
 Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala
 610 615 620
 Ile Gln Gly Val Ile Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg
 625 630 635 640
 Gly Phe Trp Ala Ala Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys
 645 650 655
 Gly Glu Lys Arg Lys Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly
 660 665 670
 Gly Ala Ala Gln Thr Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys
 675 680 685
 Gln Leu Phe Gly Ser Asp Lys Asp Phe Leu Val Ala Lys Asn His Thr
 690 695 700

Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His Ile Thr Glu Cys Ser
 705 710 715 720
 Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro Gly Ser Trp Ser His
 725 730 735
 Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr Ser His Val Ser Asn
 740 745 750
 Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu Val Lys Gly Ser Trp
 755 760 765
 Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala Ser Ser His Ser Tyr
 770 775 780
 Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala Pro Tyr Ile Lys Leu
 785 790 795 800
 Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser Glu Lys Gly Thr Glu
 805 810 815
 Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn Leu Ser Leu Pro Ile
 820 825 830
 Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn Asp Phe Ser Tyr Asp
 835 840 845
 Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg Asn Asp Pro Lys Cys
 850 855 860
 Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn
 865 870 875 880
 Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala
 885 890 895
 Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg
 900 905 910
 Gly Ser

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1200
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAT CCT AAA AAT AAA GAG TAC ACA GGG ACC ATA CTC TTT TCT GGA GAA	48
Asp Pro Lys Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu	
1 5 10 15	
AAG AGT CTA GCA AAC GAT CCT AGG GAT TTT AAA TCT ACA ATC CCT CAG	96
Lys Ser Leu Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln	
20 25 30	
AAC GTC AAC CTG TCT GCA GGA TAC TTA GTT ATT AAA GAG GGG GCC GAA	144
Asn Val Asn Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu	
35 40 45	
GTC ACA GTT TCA AAA TTC ACG CAG TCT CCA GGA TCG CAT TTA GTT TTA	192
Val Thr Val Ser Lys Phe Gln Ser Pro Gly Ser His Leu Val Leu	
50 55 60	
GAT TTA GGA ACC AAA CTG ATA GCC TCT AAG GAA GAC ATT GCC ATC ACA	240
Asp Leu Gly Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr	
65 70 75 80	
GGC CTC GCG ATA GAT ATA GAT AGC TTA AGC TCA TCC TCA ACA GCA GCT	288
Gly Leu Ala Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala	
85 90 95	
GTT ATT AAA GCA AAC ACC GCA AAT AAA CAG ATA TCC GTG ACG GAC TCT	336
Val Ile Lys Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser	
100 105 110	
ATA GAA CTT ATC TCG CCT ACT GGC AAT GCC TAT GAA GAT CTC AGA ATG	384
Ile Glu Leu Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met	
115 120 125	
AGA AAT TCA CAG ACG TTC CCT CTG CTC TCT TTA GAG CCT GGA GCC GGG	432
Arg Asn Ser Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly	
130 135 140	
GGT AGT GTG ACT GTA ACT GCT GGA GAT TTC CTA CCG GTA AGT CCC CAT	480
Gly Ser Val Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His	
145 150 155 160	
TAT GGT TTT CAA GGC AAT TGG AAA TTA GCT TGG ACA GGA ACT GGA AAC	528
Tyr Gly Phe Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn	
165 170 175	
AAA GTT GGA GAA TTC TTC TGG GAT AAA ATA AAT TAT AAG CCT AGA CCT	576
Lys Val Gly Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro	
180 185 190	
GAA AAA GAA GGA AAT TTA GTT CCT AAT ATC TTG TGG GGG AAT GCT GTA	624
Glu Lys Glu Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val	
195 200 205	
AAT GTC AGA TCC TTA ATG CAG GTT CAA GAG ACC CAT GCA TCG AGC TTA	672
Asn Val Arg Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu	
210 215 220	

CAG	ACA	GAT	CGA	GGG	CTG	TGG	ATC	GAT	GGA	ATT	GGG	AAT	TTC	TTC	CAT	720
Gln	Thr	Asp	Arg	Gly	Leu	Trp	Ile	Asp	Gly	Ile	Gly	Asn	Phe	Phe	His	
225					230					235					240	
GTA	TCT	GCC	TCC	GAA	GAC	AAT	ATA	AGG	TAC	CGT	CAT	AAC	AGC	GGT	GGA	768
Val	Ser	Ala	Ser	Glu	Asp	Asn	Ile	Arg	Tyr	Arg	His	Asn	Ser	Gly	Gly	
				245					250					255		
TAT	GTT	CTA	TCT	GTA	AAT	AAT	GAG	ATC	ACA	CCT	AAG	CAC	TAT	ACT	TCG	816
Tyr	Val	Leu	Ser	Val	Asn	Asn	Glu	Ile	Thr	Pro	Lys	His	Tyr	Thr	Ser	
			260					265					270			
ATG	GCA	TTT	TCC	CAA	CTC	TTT	AGT	AGA	GAC	AAA	GAC	TAT	GCG	GTT	TCC	864
Met	Ala	Phe	Ser	Gln	Leu	Phe	Ser	Arg	Asp	Lys	Asp	Tyr	Ala	Val	Ser	
		275						280				285				
AAC	AAC	GAA	TAC	AGA	ATG	TAT	TTA	GGA	TCG	TAT	CTC	TAT	CAA	TAT	ACA	912
Asn	Asn	Glu	Tyr	Arg	Met	Tyr	Leu	Gly	Ser	Tyr	Leu	Tyr	Gln	Tyr	Thr	
		290					295					300				
ACC	TCC	CTA	GGG	AAT	ATT	TTC	CGT	TAT	GCT	TCG	CGT	AAC	CCT	AAT	GTA	960
Thr	Ser	Leu	Gly	Asn	Ile	Phe	Arg	Tyr	Ala	Ser	Arg	Asn	Pro	Asn	Val	
305					310					315					320	
AAC	GTC	GGG	ATT	CTC	TCA	AGA	AGG	TTT	CTT	CAA	AAT	CCT	CTT	ATG	ATT	1008
Asn	Val	Gly	Ile	Leu	Ser	Arg	Arg	Phe	Leu	Gln	Asn	Pro	Leu	Met	Ile	
				325					330					335		
TTT	CAT	TTT	TTG	TGT	GCT	TAT	GGT	CAT	GCC	ACC	AAT	GAT	ATG	AAA	ACA	1056
Phe	His	Phe	Leu	Cys	Ala	Tyr	Gly	His	Ala	Thr	Asn	Asp	Met	Lys	Thr	
			340					345					350			
GAC	TAC	GCA	AAT	TTC	CCT	ATG	GTG	AAA	AAC	AGC	TGG	AGA	AAC	AAT	TGT	1104
Asp	Tyr	Ala	Asn	Phe	Pro	Met	Val	Lys	Asn	Ser	Trp	Arg	Asn	Asn	Cys	
		355					360					365				
TGG	GCT	ATA	AAA	TGC	GGA	GGG	AGC	ATG	CCT	CTA	TTG	GTA	TTT	GAA	AAC	1152
Trp	Ala	Ile	Lys	Cys	Gly	Gly	Ser	Met	Pro	Leu	Leu	Val	Phe	Glu	Asn	
		370				375						380				
GGA	AAA	CTT	TTC	CAA	GGT	GCC	ATC	CCA	TTT	ATG	AAA	CTA	CAA	TTA	GTT	1200
Gly	Lys	Leu	Phe	Gln	Gly	Ala	Ile	Pro	Phe	Met	Lys	Leu	Gln	Leu	Val	
385					390					395					400	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asp Pro Lys Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu
 1 5 10 15
 Lys Ser Leu Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln
 20 25 30
 Asn Val Asn Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu
 35 40 45
 Val Thr Val Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu
 50 55 60
 Asp Leu Gly Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr
 65 70 75 80
 Gly Leu Ala Ile Asp Ile Asp Ser Leu Ser Ser Ser Thr Ala Ala
 85 90 95
 Val Ile Lys Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser
 100 105 110
 Ile Glu Leu Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met
 115 120 125
 Arg Asn Ser Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly
 130 135 140
 Gly Ser Val Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His
 145 150 155 160
 Tyr Gly Phe Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn
 165 170 175
 Lys Val Gly Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro
 180 185 190
 Glu Lys Glu Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val
 195 200 205
 Asn Val Arg Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu
 210 215 220
 Gln Thr Asp Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His
 225 230 235 240
 Val Ser Ala Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly
 245 250 255
 Tyr Val Leu Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser
 260 265 270
 Met Ala Phe Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser
 275 280 285
 Asn Asn Glu Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr
 290 295 300

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Thr Ser Leu Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val
305                      310                      315                      320

Asn Val Gly Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile
                      325                      330                      335

Phe His Phe Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr
                      340                      345                      350

Asp Tyr Ala Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys
                      355                      360                      365

Trp Ala Ile Lys Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn
370                      375                      380

Gly Lys Leu Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val
385                      390                      395                      400

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1830
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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GAT CTC ACA TTA GGG AGT CGT GAC AGT TAT AAT GGT GAT ACA AGC ACC      48
Asp Leu Thr Leu Gly Ser Arg Asp Ser Tyr Asn Gly Asp Thr Ser Thr
  1                      5                      10                      15

ACA GAA TTT ACT CCT AAA GCG GCA ACT TCT GAT GCT AGT GGC ACG ACC      96
Thr Glu Phe Thr Pro Lys Ala Ala Thr Ser Asp Ala Ser Gly Thr Thr
                      20                      25                      30

TAT ATT CTC GAT GGG GAT GTC TCG ATA AGC CAA GCA GGG AAA CAA ACG     144
Tyr Ile Leu Asp Gly Asp Val Ser Ile Ser Gln Ala Gly Lys Gln Thr
                      35                      40                      45

AGC TTA ACC ACA AGT TGT TTT TCT AAC ACT GCA GGA AAT CTT ACC TTC     192
Ser Leu Thr Thr Ser Cys Phe Ser Asn Thr Ala Gly Asn Leu Thr Phe
                      50                      55                      60

TTA GGG AAC GGA TTT TCT CTT CAT TTT GAC AAT ATT ATT TCG TCT ACT     240
Leu Gly Asn Gly Phe Ser Leu His Phe Asp Asn Ile Ile Ser Ser Thr
                      65                      70                      75                      80

GTT GCA GGT GTT GTT GTT AGC AAT ACA GCA GCT TCT GGG ATT ACG AAA     288
Val Ala Gly Val Val Val Ser Asn Thr Ala Ala Ser Gly Ile Thr Lys

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				85				90				95							
TTC	TCA	GGA	TTT	TCA	ACT	CTT	CGG	ATG	CTT	GCA	GCT	CCT	AGG	ACC	ACA	336			
Phe	Ser	Gly	Phe	Ser	Thr	Leu	Arg	Met	Leu	Ala	Ala	Pro	Arg	Thr	Thr				
100								105				110							
GGT	AAA	GGA	GCC	ATT	AAA	ATT	ACC	GAT	GGT	CTG	GTG	TTT	GAG	AGT	ATA	384			
Gly	Lys	Gly	Ala	Ile	Lys	Ile	Thr	Asp	Gly	Leu	Val	Phe	Glu	Ser	Ile				
115								120				125							
GGG	AAT	CTT	GAT	CCG	ATT	ACT	GTA	ACA	GGA	TCG	ACA	TCT	GTT	GCT	GAT	432			
Gly	Asn	Leu	Asp	Pro	Ile	Thr	Val	Thr	Gly	Ser	Thr	Ser	Val	Ala	Asp				
130								135				140							
GCT	CTC	AAT	ATT	AAT	AGC	CCT	GAT	ACT	GGA	GAT	AAC	AAA	GAG	TAT	ACG	480			
Ala	Leu	Asn	Ile	Asn	Ser	Pro	Asp	Thr	Gly	Asp	Asn	Lys	Glu	Tyr	Thr				
145				150				155				160							
GGA	ACC	ATA	GTC	TTT	TCT	GGA	GAG	AAG	CTC	ACG	GAG	GCA	GAA	GCT	AAA	528			
Gly	Thr	Ile	Val	Phe	Ser	Gly	Glu	Lys	Leu	Thr	Glu	Ala	Glu	Ala	Lys				
165								170				175							
GAT	GAG	AAG	AAC	CGC	ACT	TCT	AAA	TTA	CTT	CAA	AAT	GTT	GCT	TTT	AAA	576			
Asp	Glu	Lys	Asn	Arg	Thr	Ser	Lys	Leu	Leu	Gln	Asn	Val	Ala	Phe	Lys				
180								185				190							
AAT	GGG	ACT	GTA	GTT	TTA	AAA	GGT	GAT	GTC	GTT	TTA	AGT	GCG	AAC	GGT	624			
Asn	Gly	Thr	Val	Val	Leu	Lys	Gly	Asp	Val	Val	Leu	Ser	Ala	Asn	Gly				
195								200				205							
TTC	TCT	CAG	GAT	GCA	AAC	TCT	AAG	TTG	ATT	ATG	GAT	TTA	GGG	ACG	TCG	672			
Phe	Ser	Gln	Asp	Ala	Asn	Ser	Lys	Leu	Ile	Met	Asp	Leu	Gly	Thr	Ser				
210								215				220							
TTG	GTT	GCA	AAC	ACC	GAA	AGT	ATC	GAG	TTA	ACG	AAT	TTG	GAA	ATT	AAT	720			
Leu	Val	Ala	Asn	Thr	Glu	Ser	Ile	Glu	Leu	Thr	Asn	Leu	Glu	Ile	Asn				
225				230				235				240							
ATA	GAC	TCT	CTC	AGG	AAC	GGG	AAA	AAG	ATA	AAA	CTC	AGT	GCT	GCC	ACA	768			
Ile	Asp	Ser	Leu	Arg	Asn	Gly	Lys	Lys	Ile	Lys	Leu	Ser	Ala	Ala	Thr				
245								250				255							
GCT	CAG	AAA	GAT	ATT	CGT	ATA	GAT	CGT	CCT	GTT	GTA	CTG	GCA	ATT	AGC	816			
Ala	Gln	Lys	Asp	Ile	Arg	Ile	Asp	Arg	Pro	Val	Val	Leu	Ala	Ile	Ser				
260								265				270							
GAT	GAG	AGT	TTT	TAT	CAA	AAT	GGC	TTT	TTG	AAT	GAG	GAC	CAT	TCC	TAT	864			
Asp	Glu	Ser	Phe	Tyr	Gln	Asn	Gly	Phe	Leu	Asn	Glu	Asp	His	Ser	Tyr				
275								280				285							
GAT	GGG	ATT	CTT	GAG	TTA	GAT	GCT	GGG	AAA	GAC	ATC	GTG	ATT	TCT	GCA	912			
Asp	Gly	Ile	Leu	Glu	Leu	Asp	Ala	Gly	Lys	Asp	Ile	Val	Ile	Ser	Ala				
290								295				300							
GAT	TCT	CGC	AGT	ATA	GAT	GCT	GTA	CAA	TCT	CCG	TAT	GGC	TAT	CAG	GGA	960			
Asp	Ser	Arg	Ser	Ile	Asp	Ala	Val	Gln	Ser	Pro	Tyr	Gly	Tyr	Gln	Gly				
305				310				315				320							

AAG	TGG	ACG	ATC	AAT	TGG	TCT	ACT	GAT	GAT	AAG	AAA	GCT	ACG	GTT	TCT	1008
Lys	Trp	Thr	Ile	Asn	Trp	Ser	Thr	Asp	Asp	Lys	Lys	Ala	Thr	Val	Ser	
				325					330						335	
TGG	GCG	AAG	CAG	AGT	TTT	AAT	CCC	ACT	GCT	GAG	CAG	GAG	GCT	CCG	TTA	1056
Trp	Ala	Lys	Gln	Ser	Phe	Asn	Pro	Thr	Ala	Glu	Gln	Glu	Ala	Pro	Leu	
			340					345					350			
GTT	CCT	AAT	CTT	CTT	TGG	GGT	TCT	TTT	ATA	GAT	GTT	CGT	TCC	TTC	CAG	1104
Val	Pro	Asn	Leu	Leu	Trp	Gly	Ser	Phe	Ile	Asp	Val	Arg	Ser	Phe	Gln	
		355					360					365				
AAT	TTT	ATA	GAG	CTA	GGT	ACT	GAA	GGT	GCT	CCT	TAC	GAA	AAG	AGA	TTT	1152
Asn	Phe	Ile	Glu	Leu	Gly	Thr	Glu	Gly	Ala	Pro	Tyr	Glu	Lys	Arg	Phe	
	370					375					380					
TGG	GTT	GCA	GGC	ATT	TCC	AAT	GTT	TTG	CAT	AGG	AGC	GGT	CGT	GAA	AAT	1200
Trp	Val	Ala	Gly	Ile	Ser	Asn	Val	Leu	His	Arg	Ser	Gly	Arg	Glu	Asn	
385					390					395					400	
CAA	AGG	AAA	TTC	CGT	CAT	GTG	AGT	GGA	GGT	GCT	GTA	GTA	GGT	GCT	AGC	1248
Gln	Arg	Lys	Phe	Arg	His	Val	Ser	Gly	Gly	Ala	Val	Val	Gly	Ala	Ser	
				405					410					415		
ACG	AGG	ATG	CCG	GGT	GGT	GAT	ACC	TTG	TCT	CTG	GGT	TTT	GCT	CAG	CTC	1296
Thr	Arg	Met	Pro	Gly	Gly	Asp	Thr	Leu	Ser	Leu	Gly	Phe	Ala	Gln	Leu	
			420					425					430			
TTT	GCG	CGT	GAC	AAA	GAC	TAC	TTT	ATG	AAT	ACC	AAT	TTC	GCA	AAG	ACC	1344
Phe	Ala	Arg	Asp	Lys	Asp	Tyr	Phe	Met	Asn	Thr	Asn	Phe	Ala	Lys	Thr	
		435					440					445				
TAC	GCA	GGA	TCT	TTA	CGT	TTG	CAG	CAC	GAT	GCT	TCC	CTA	TAC	TCT	GTG	1392
Tyr	Ala	Gly	Ser	Leu	Arg	Leu	Gln	His	Asp	Ala	Ser	Leu	Tyr	Ser	Val	
	450					455					460					
GTG	AGT	ATC	CTT	TTA	GGA	GAG	GGA	GGA	CTC	CGC	GAG	ATC	CTG	TTG	CCT	1440
Val	Ser	Ile	Leu	Leu	Gly	Glu	Gly	Gly	Leu	Arg	Glu	Ile	Leu	Leu	Pro	
465					470				475						480	
TAT	GTT	TCC	AAT	ACT	CTG	CCG	TGC	TCT	TTC	TAT	GGG	CAG	CTT	AGC	TAC	1488
Tyr	Val	Ser	Asn	Thr	Leu	Pro	Cys	Ser	Phe	Tyr	Gly	Gln	Leu	Ser	Tyr	
			485					490						495		
GGC	CAT	ACG	GAT	CAT	CGC	ATG	AAG	ACC	GAG	TCT	CTA	CCC	CCC	CCC	CCC	1536
Gly	His	Thr	Asp	His	Arg	Met	Lys	Thr	Glu	Ser	Leu	Pro	Pro	Pro	Pro	
			500					505					510			
CCG	ACG	CTC	TCG	ACG	GAT	CAT	ACT	TCT	TGG	GGA	GGA	TAT	GTC	TGG	GCT	1584
Pro	Thr	Leu	Ser	Thr	Asp	His	Thr	Ser	Trp	Gly	Gly	Tyr	Val	Trp	Ala	
			515				520					525				
GGA	GAG	CTG	GGA	ACT	CGA	GTT	GCT	GTT	GAA	AAT	ACC	AGC	GGC	AGA	GGA	1632
Gly	Glu	Leu	Gly	Thr	Arg	Val	Ala	Val	Glu	Asn	Thr	Ser	Gly	Arg	Gly	
	530					535					540					
TTT	TTC	CGA	GAG	TAC	ACT	CCA	TTT	GTA	AAA	GTC	CAA	GCT	GTT	TAC	TCG	1680
Phe	Phe	Arg	Glu	Tyr	Thr	Pro	Phe	Val	Lys	Val	Gln	Ala	Val	Tyr	Ser	

545	550	555	560	
CGC CAA GAT AGC TTT GTT GAA CTA GGA GCT ATC AGT CGT GAT TTT AGT				1728
Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser				
	565	570	575	
GAT TCG CAT CTT TAT AAC CTT GCG ATT CCT CTT GGA ATC AAG TTA GAG				1776
Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu				
	580	585	590	
AAA CGG TTT GCA GAG CAA TAT TAT CAT GTT GTT GCG ATG TAT TCT CCA				1824
Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro				
	595	600	605	
GAT GTT				1830
Asp Val				
610				

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp	Leu	Thr	Leu	Gly	Ser	Arg	Asp	Ser	Tyr	Asn	Gly	Asp	Thr	Ser	Thr
1				5					10					15	
Thr	Glu	Phe	Thr	Pro	Lys	Ala	Ala	Thr	Ser	Asp	Ala	Ser	Gly	Thr	Thr
			20					25					30		
Tyr	Ile	Leu	Asp	Gly	Asp	Val	Ser	Ile	Ser	Gln	Ala	Gly	Lys	Gln	Thr
		35				40						45			
Ser	Leu	Thr	Thr	Ser	Cys	Phe	Ser	Asn	Thr	Ala	Gly	Asn	Leu	Thr	Phe
	50					55					60				
Leu	Gly	Asn	Gly	Phe	Ser	Leu	His	Phe	Asp	Asn	Ile	Ile	Ser	Ser	Thr
65					70					75					80
Val	Ala	Gly	Val	Val	Val	Ser	Asn	Thr	Ala	Ala	Ser	Gly	Ile	Thr	Lys
				85					90					95	
Phe	Ser	Gly	Phe	Ser	Thr	Leu	Arg	Met	Leu	Ala	Ala	Pro	Arg	Thr	Thr
			100					105					110		
Gly	Lys	Gly	Ala	Ile	Lys	Ile	Thr	Asp	Gly	Leu	Val	Phe	Glu	Ser	Ile
		115					120					125			
Gly	Asn	Leu	Asp	Pro	Ile	Thr	Val	Thr	Gly	Ser	Thr	Ser	Val	Ala	Asp

130	135	140
Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr		
145	150	155 160
Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys		
	165	170 175
Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys		
	180	185 190
Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly		
	195	200 205
Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser		
	210	215 220
Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn		
	225	230 235 240
Ile Asp Ser Leu Arg Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr		
	245	250 255
Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser		
	260	265 270
Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr		
	275	280 285
Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala		
	290	295 300
Asp Ser Arg Ser Ile Asp Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly		
	305	310 315 320
Lys Trp Thr Ile Asn Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser		
	325	330 335
Trp Ala Lys Gln Ser Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu		
	340	345 350
Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Ser Phe Gln		
	355	360 365
Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe		
	370	375 380
Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn		
	385	390 395 400
Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser		
	405	410 415
Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu		
	420	425 430
Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr		
	435	440 445

Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val
 450 455 460
 Val Ser Ile Leu Leu Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro
 465 470 475 480
 Tyr Val Ser Asn Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr
 485 490 495
 Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro
 500 505 510
 Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala
 515 520 525
 Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly
 530 535 540
 Phe Phe Arg Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ser
 545 550 555 560
 Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser
 565 570 575
 Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu
 580 585 590
 Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro
 595 600 605
 Asp Val
 610